97965

STIC-Biotech/ChemLib

From: Fredman, Jeffrey
Sent: Wednesday, July 02, 2003 12:51 PM
To: STIC-Biotech/ChemLib
Cc: Schultz, James
Subject: FW: Rush Sequence search request 09/780,929

PLEASE RUSH.

I Approve.

Jeff Fredman

CRISE

-----Original Message-----
From: Schultz, James
Sent: Wednesday, July 02, 2003 9:38 AM
To: Fredman, Jeffrey
Subject: Rush Sequence search request 09/780,929

Dear Jeff,
Would you please approve the rush sequence search below? This case has already been searched and is ready for allowance, but my SPE wants it searched one more way before we pass it out.
Thanks,
Doug Schultz

Dear STIC-biotech searchers,
Could you please run a length limited nucleotide sequence search on SEQ ID NOS 97 (15 nt long) and 98 (18 nt long) in the above entitled case, where the maximum size of the returned hit is no longer than 60 nucleotides? I need both sequences searched in the **interference** databases as well.
Thanks,
Doug Schultz

J. Douglas Schultz, Ph.D.
AU 1635 (Biotechnology)
Patent Examiner
United States Patent and Trademark Office
(703) 308-9355
(703) 746-3973 (fax)
Office: CM1 12E18
Mail: CM1 11E12

Searcher:_____
Phone:_____
Location:_____
Date Picked Up:_____
Searcher Prep/Review:_____
Clerical:_____
Online time:_____

TYPE OF SEARCH:
NA Sequences:_____
AA Sequences:_____
Structures:_____
Bibliographic:_____
Litigation:_____
Full text:_____
Patent Family:_____
Other:_____

VENDOR/COST (where applic.)
STN:_____
DIALOG:_____
Questel/Orbit:_____
DRLink:_____
Lexis/Nexis:_____
Sequence Sys.:_____
WWW/Internet:_____
Other (specify):_____

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: July 6, 2003, 14:51:21 ; Search time 520.455 Seconds
(without alignments)
206.249 Million cell updates/sec

Title: US-09-780-929-97
Perfect score: 15
Sequence: 1 agauaacgugaagau 15

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 8255821 seqs, 3578102051 residues

Total number of hits satisfying chosen parameters: 9359164

Minimum DB seq length: 0
Maximum DB seq length: 60

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending_Patents_NA_New:*
1: /cgn2_6/ptodata/2/pna/PCT_NEW_COMB.seq:*
2: /cgn2_6/ptodata/2/pna/PCT_NEW_COMB.seq4:*
3: /cgn2_6/ptodata/2/pna/US06_NEW_COMB.seq:*
4: /cgn2_6/ptodata/2/pna/US06_NEW_COMB.seq4:*
5: /cgn2_6/ptodata/2/pna/US07_NEW_COMB.seq:*
6: /cgn2_6/ptodata/2/pna/US07_NEW_COMB.seq4:*
7: /cgn2_6/ptodata/2/pna/US08_NEW_COMB.seq:*
8: /cgn2_6/ptodata/2/pna/US08_NEW_COMB.seq4:*
9: /cgn2_6/ptodata/2/pna/US09_NEW_COMB.seq:*
10: /cgn2_6/ptodata/2/pna/US09_NEW_COMB.seq2:*
11: /cgn2_6/ptodata/2/pna/US09_NEW_COMB.seq3:*
12: /cgn2_6/ptodata/2/pna/US09_NEW_COMB.seq4:*
13: /cgn2_6/ptodata/2/pna/US10_NEW_COMB.seq:*
14: /cgn2_6/ptodata/2/pna/US10_NEW_COMB.seq2:*
15: /cgn2_6/ptodata/2/pna/US10_NEW_COMB.seq3:*
16: /cgn2_6/ptodata/2/pna/US10_NEW_COMB.seq4:*
17: /cgn2_6/ptodata/2/pna/US60_NEW_COMB.seq:*
18: /cgn2_6/ptodata/2/pna/US60_NEW_COMB.seq2:*
19: /cgn2_6/ptodata/2/pna/US60_NEW_COMB.seq3:*
20: /cgn2_6/ptodata/2/pna/US60_NEW_COMB.seq4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
c	1	13.4	89.3	25	14	US-10-355-577-24855	Sequence 24855, A
c	2	13.4	89.3	25	18	US-60-427-836-243678	Sequence 243678,
c	3	13	86.7	25	14	US-10-355-577-179244	Sequence 179244,
	4	13	86.7	25	18	US-60-427-836-118114	Sequence 118114,
c	5	12.4	82.7	23	14	US-10-310-188-75880	Sequence 75880, A
c	6	12.4	82.7	25	10	US-09-660-222-72811	Sequence 72811, A
c	7	12.4	82.7	25	10	US-09-660-222-72812	Sequence 72812, A
c	8	12.4	82.7	25	11	US-09-953-570-48322	Sequence 48322, A
c	9	12.4	82.7	25	11	US-09-953-570-48329	Sequence 48329, A
c	10	12.4	82.7	25	11	US-09-954-445A-10200	Sequence 10200, A
	11	12.4	82.7	25	11	US-09-954-445A-16612	Sequence 16612, A
	12	12.4	82.7	25	11	US-09-954-445A-16620	Sequence 16620, A
	13	12.4	82.7	25	11	US-09-954-445A-50048	Sequence 50048, A
	14	12.4	82.7	25	14	US-10-355-577-40591	Sequence 40591, A
c	15	12.4	82.7	25	14	US-10-355-577-366476	Sequence 366476,
c	16	12.4	82.7	25	14	US-10-355-577-485354	Sequence 485354,
c	17	12.4	82.7	25	14	US-10-355-577-511942	Sequence 511942,
c	18	12.4	82.7	25	14	US-10-355-577-735345	Sequence 735345,
c	19	12.4	82.7	25	14	US-10-355-577-834196	Sequence 834196,
c	20	12.4	82.7	25	14	US-10-355-577-907847	Sequence 907847,
c	21	12.4	82.7	25	18	US-60-427-808-475949	Sequence 475949,
	22	12.4	82.7	25	18	US-60-427-808-568077	Sequence 568077,
	23	12.4	82.7	25	18	US-60-427-808-695630	Sequence 695630,
c	24	12.4	82.7	25	18	US-60-427-808-928248	Sequence 928248,
c	25	12.4	82.7	25	18	US-60-427-836-166264	Sequence 166264,
c	26	12.4	82.7	25	18	US-60-427-836-525766	Sequence 525766,
c	27	12.4	82.7	25	18	US-60-427-836-674310	Sequence 674310,
c	28	12.4	82.7	25	19	US-60-469-545-95587	Sequence 95587, A
c	29	12.4	82.7	25	19	US-60-469-545-96568	Sequence 96568, A
	30	12.4	82.7	25	19	US-60-469-545-141609	Sequence 141609,
	31	12.4	82.7	25	19	US-60-469-545-142590	Sequence 142590,
	32	12.4	82.7	25	20	US-60-475-871-165169	Sequence 165169,
	33	12.4	82.7	41	15	US-10-408-085-133	Sequence 133, App
	34	12.4	82.7	41	15	US-10-408-085-359	Sequence 359, App
c	35	12	80.0	22	14	US-10-310-188-49187	Sequence 49187, A
c	36	12	80.0	25	10	US-09-660-222-100324	Sequence 100324,
c	37	12	80.0	25	11	US-09-953-570-45886	Sequence 45886, A
c	38	12	80.0	25	11	US-09-953-570-45892	Sequence 45892, A
c	39	12	80.0	25	14	US-10-098-263B-27903	Sequence 27903, A
c	40	12	80.0	25	14	US-10-355-577-53971	Sequence 53971, A
c	41	12	80.0	25	14	US-10-355-577-143487	Sequence 143487,
c	42	12	80.0	25	14	US-10-355-577-518580	Sequence 518580,
c	43	12	80.0	25	14	US-10-355-577-653875	Sequence 653875,
c	44	12	80.0	25	14	US-10-355-577-827041	Sequence 827041,
c	45	12	80.0	25	14	US-10-355-577-899636	Sequence 899636,

ALIGNMENTS

RESULT 1
US-10-355-577-24855/c
; Sequence 24855, Application US/10355577
; GENERAL INFORMATION:
; APPLICANT: Mittmann, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Probes: HG-U133
; FILE REFERENCE: 3121
; CURRENT APPLICATION NUMBER: US/10/355,577
; CURRENT FILING DATE: 2003-01-31
; NUMBER OF SEQ ID NOS: 997516
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 24855
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-355-577-24855

Query Match 89.3%; Score 13.4; DB 14; Length 25;
Best Local Similarity 73.3%; Pred. No. 1.9e+03;
Matches 11; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

```
Qy          1 AGAUAACGUGAAGAU 15
              |||:||||:| |||:
Db         25 AGATAACGTGCAGAT 11
```

RESULT 2
US-60-427-836-243678/c
; Sequence 243678, Application US/60427836
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527
; CURRENT APPLICATION NUMBER: US/60/427,836
; CURRENT FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 699466

```
;  SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 243678
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Rattus norvegicus
US-60-427-836-243678

  Query Match             89.3%;  Score 13.4;  DB 18;  Length 25;
  Best Local Similarity   73.3%;  Pred. No. 1.9e+03;
  Matches   11;  Conservative    3;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 AGAUAACGUGAAGAU 15
              |||:|| |:||||:
Db         21 AGATAAAGTGAAGAT 7


RESULT 3
US-10-355-577-179244/c
; Sequence 179244, Application US/10355577
; GENERAL INFORMATION:
;  APPLICANT: Mittmann, Michael
;  TITLE OF INVENTION: Methods of Genetic Analysis of Probes: HG-U133
;  FILE REFERENCE: 3121
;  CURRENT APPLICATION NUMBER: US/10/355,577
;  CURRENT FILING DATE:  2003-01-31
;  NUMBER OF SEQ ID NOS: 997516
;  SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 179244
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Homo sapien
US-10-355-577-179244

  Query Match             86.7%;  Score 13;  DB 14;  Length 25;
  Best Local Similarity   84.6%;  Pred. No. 3.1e+03;
  Matches   11;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 GAUAACGUGAAGA 14
              ||:||||:|||||
Db         22 GATAACGTGAAGA 10


RESULT 4
US-60-427-836-118114
; Sequence 118114, Application US/60427836
; GENERAL INFORMATION:
;  APPLICANT: Xue Mei Zhou
;  TITLE OF INVENTION: Methods of Genetic Analysis of Rat
;  FILE REFERENCE: 3527
;  CURRENT APPLICATION NUMBER: US/60/427,836
;  CURRENT FILING DATE:  2002-11-20
;  NUMBER OF SEQ ID NOS: 699466
;  SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 118114
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Rattus norvegicus
US-60-427-836-118114

  Query Match             86.7%;  Score 13;  DB 18;  Length 25;
  Best Local Similarity   84.6%;  Pred. No. 3.1e+03;
  Matches   11;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAUAACGUGAAG 13
              |||:||||:||||
Db          1 AGATAACGTGAAG 13


RESULT 5
US-10-310-188-75880/c
; Sequence 75880, Application US/10310188
; GENERAL INFORMATION:
;  APPLICANT: RosettaGemonics
;  TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY
;  TITLE OF INVENTION:  USES THEREOF
;  FILE REFERENCE: 47487
;  CURRENT APPLICATION NUMBER: US/10/310,188
;  CURRENT FILING DATE:  2002-12-19
;  NUMBER OF SEQ ID NOS: 86841
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 75880
;   LENGTH: 23
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-310-188-75880

  Query Match             82.7%;  Score 12.4;  DB 14;  Length 23;
  Best Local Similarity   78.6%;  Pred. No. 6.7e+03;
  Matches   11;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 AGAUAACGUGAAGA 14
              | |:||||:|||||
Db         23 AAATAACGTGAAGA 10


RESULT 6
US-09-660-222-72811/c
; Sequence 72811, Application US/09660222
; GENERAL INFORMATION:
;  APPLICANT: Mittmann et al.
;  APPLICANT:  Affymetrix, Inc.
;  TITLE OF INVENTION: Methods of Genetic Analysis of Human
;  FILE REFERENCE: 3102.1
;  CURRENT APPLICATION NUMBER: US/09/660,222
;  CURRENT FILING DATE:  2000-09-12
;  PRIOR APPLICATION NUMBER: 60/164,973
;  PRIOR FILING DATE: 1999-11-11
;  NUMBER OF SEQ ID NOS: 140981
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 72811
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Homo Sapiens
;  PUBLICATION INFORMATION:
;   DATABASE ACCESSION NUMBER: GenBank S80343
US-09-660-222-72811

  Query Match             82.7%;  Score 12.4;  DB 10;  Length 25;
  Best Local Similarity   78.6%;  Pred. No. 6.7e+03;
  Matches   11;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 AGAUAACGUGAAGA 14
              |||:||||:| |||
Db         16 AGATAACGTGCAGA 3


RESULT 7
US-09-660-222-72812/c
; Sequence 72812, Application US/09660222
; GENERAL INFORMATION:
;  APPLICANT: Mittmann et al.
;  APPLICANT:  Affymetrix, Inc.
;  TITLE OF INVENTION: Methods of Genetic Analysis of Human
;  FILE REFERENCE: 3102.1
;  CURRENT APPLICATION NUMBER: US/09/660,222
;  CURRENT FILING DATE:  2000-09-12
;  PRIOR APPLICATION NUMBER: 60/164,973
;  PRIOR FILING DATE: 1999-11-11
;  NUMBER OF SEQ ID NOS: 140981
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 72812
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Homo Sapiens
;  PUBLICATION INFORMATION:
;   DATABASE ACCESSION NUMBER: GenBank S80343
```

US-09-660-222-72812

Query Match 82.7%; Score 12.4; DB 10; Length 25;
Best Local Similarity 78.6%; Pred. No. 6.7e+03;
Matches 11; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

```
Qy          1 AGAUAACGUGAAGA 14
              |||:||||:| |||
Db         22 AGATAACGTGCAGA 9
```

RESULT 8
US-09-953-570-48322/c
; Sequence 48322, Application US/09953570
; GENERAL INFORMATION:
; APPLICANT: Mittmann, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Yeast
; FILE REFERENCE: 3110.1
; CURRENT APPLICATION NUMBER: US/09/953,570
; CURRENT FILING DATE: 2001-09-13
; PRIOR APPLICATION NUMBER: 60/232,638
; PRIOR FILING DATE: 2000-09-14
; NUMBER OF SEQ ID NOS: 138410
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 48322
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces Cerevisiae
US-09-953-570-48322

Query Match 82.7%; Score 12.4; DB 11; Length 25;
Best Local Similarity 78.6%; Pred. No. 6.7e+03;
Matches 11; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

```
Qy          1 AGAUAACGUGAAGA 14
              |||:||||:| |||
Db         14 AGATAACGTGTAGA 1
```

RESULT 9
US-09-953-570-48329/c
; Sequence 48329, Application US/09953570
; GENERAL INFORMATION:
; APPLICANT: Mittmann, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Yeast
; FILE REFERENCE: 3110.1
; CURRENT APPLICATION NUMBER: US/09/953,570
; CURRENT FILING DATE: 2001-09-13
; PRIOR APPLICATION NUMBER: 60/232,638
; PRIOR FILING DATE: 2000-09-14
; NUMBER OF SEQ ID NOS: 138410
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 48329
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces Cerevisiae
US-09-953-570-48329

Query Match 82.7%; Score 12.4; DB 11; Length 25;
Best Local Similarity 78.6%; Pred. No. 6.7e+03;
Matches 11; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

```
Qy          1 AGAUAACGUGAAGA 14
              |||:||||:| |||
Db         20 AGATAACGTGTAGA 7
```

RESULT 10
US-09-954-445A-10200/c
; Sequence 10200, Application US/09954445A
; GENERAL INFORMATION:
; APPLICANT: Mittmann, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Arabidopsis Thaliana
; FILE REFERENCE: 3116.1
; CURRENT APPLICATION NUMBER: US/09/954,445A
; CURRENT FILING DATE: 2000-09-17
; PRIOR APPLICATION NUMBER: 60/233,620
; PRIOR FILING DATE: 2000-09-18
; NUMBER OF SEQ ID NOS: 131820
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 10200
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-954-445A-10200

Query Match 82.7%; Score 12.4; DB 11; Length 25;
Best Local Similarity 78.6%; Pred. No. 6.7e+03;
Matches 11; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

```
Qy          1 AGAUAACGUGAAGA 14
              |||:|| |:|||||
Db         17 AGATAAAGTGAAGA 4
```

RESULT 11
US-09-954-445A-16612
; Sequence 16612, Application US/09954445A
; GENERAL INFORMATION:
; APPLICANT: Mittmann, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Arabidopsis Thaliana
; FILE REFERENCE: 3116.1
; CURRENT APPLICATION NUMBER: US/09/954,445A
; CURRENT FILING DATE: 2000-09-17
; PRIOR APPLICATION NUMBER: 60/233,620
; PRIOR FILING DATE: 2000-09-18
; NUMBER OF SEQ ID NOS: 131820
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 16612
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-954-445A-16612

Query Match 82.7%; Score 12.4; DB 11; Length 25;
Best Local Similarity 71.4%; Pred. No. 6.7e+03;
Matches 10; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

```
Qy          2 GAUAACGUGAAGAU 15
              ||:||||:||| |:
Db          6 GATAACGTGAATAT 19
```

RESULT 12
US-09-954-445A-16620
; Sequence 16620, Application US/09954445A
; GENERAL INFORMATION:
; APPLICANT: Mittmann, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Arabidopsis Thaliana
; FILE REFERENCE: 3116.1
; CURRENT APPLICATION NUMBER: US/09/954,445A
; CURRENT FILING DATE: 2000-09-17
; PRIOR APPLICATION NUMBER: 60/233,620
; PRIOR FILING DATE: 2000-09-18
; NUMBER OF SEQ ID NOS: 131820
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 16620
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-954-445A-16620

Query Match 82.7%; Score 12.4; DB 11; Length 25;
Best Local Similarity 71.4%; Pred. No. 6.7e+03;
Matches 10; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

```
Qy          2 GAUAACGUGAAGAU 15
              ||:||||:||| |:
Db          1 GATAACGTGAATAT 14


RESULT 13
US-09-954-445A-50048
; Sequence 50048, Application US/09954445A
; GENERAL INFORMATION:
;  APPLICANT: Mittmann, Michael
;  TITLE OF INVENTION: Methods of Genetic Analysis of Arabidopsis Thaliana
;  FILE REFERENCE: 3116.1
;  CURRENT APPLICATION NUMBER: US/09/954,445A
;  CURRENT FILING DATE:  2000-09-17
;  PRIOR APPLICATION NUMBER: 60/233,620
;  PRIOR FILING DATE: 2000-09-18
;  NUMBER OF SEQ ID NOS: 131820
;  SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 50048
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Arabidopsis thaliana
US-09-954-445A-50048

  Query Match             82.7%;  Score 12.4;  DB 11;  Length 25;
  Best Local Similarity   71.4%;  Pred. No. 6.7e+03;
  Matches   10;  Conservative    3;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 GAUAACGUGAAGAU 15
              ||: |||:|||||:
Db          6 GATTACGTGAAGAT 19


RESULT 14
US-10-355-577-40591
; Sequence 40591, Application US/10355577
; GENERAL INFORMATION:
;  APPLICANT: Mittmann, Michael
;  TITLE OF INVENTION: Methods of Genetic Analysis of Probes: HG-U133
;  FILE REFERENCE: 3121
;  CURRENT APPLICATION NUMBER: US/10/355,577
;  CURRENT FILING DATE:  2003-01-31
;  NUMBER OF SEQ ID NOS: 997516
;  SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 40591
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Homo sapien
US-10-355-577-40591

  Query Match             82.7%;  Score 12.4;  DB 14;  Length 25;
  Best Local Similarity   85.7%;  Pred. No. 6.7e+03;
  Matches   12;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 AGAUAACGUGAAGA 14
              ||| ||||:|||||
Db          2 AGAGAACGTGAAGA 15


RESULT 15
US-10-355-577-366476/c
; Sequence 366476, Application US/10355577
; GENERAL INFORMATION:
;  APPLICANT: Mittmann, Michael
;  TITLE OF INVENTION: Methods of Genetic Analysis of Probes: HG-U133
;  FILE REFERENCE: 3121
;  CURRENT APPLICATION NUMBER: US/10/355,577
;  CURRENT FILING DATE:  2003-01-31
;  NUMBER OF SEQ ID NOS: 997516
;  SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 366476
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Homo sapien
US-10-355-577-366476

  Query Match             82.7%;  Score 12.4;  DB 14;  Length 25;
  Best Local Similarity   78.6%;  Pred. No. 6.7e+03;
  Matches   11;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 AGAUAACGUGAAGA 14
              |||:||||:| |||
Db         18 AGATAACGTGCAGA 5


Search completed: July  6, 2003, 16:49:13
Job time : 522.455 secs
```

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: July 6, 2003, 14:26:16 ; Search time 493.182 Seconds
(without alignments)
885.154 Million cell updates/sec

Title: US-09-780-929-97
Perfect score: 15
Sequence: 1 agauaacgugaagau 15

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 897812

Minimum DB seq length: 0
Maximum DB seq length: 60

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vi:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htg_mus:*
34: em_htg_pln:*
35: em_htg_rod:*
36: em_htg_mam:*
37: em_htg_vrt:*
38: em_sy:*
39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	15	100.0	15	6	AX214295	AX214295 Sequence
2	15	100.0	27	6	AX214239	AX214239 Sequence
3	15	100.0	28	6	AX214237	AX214237 Sequence
4	15	100.0	28	6	AX214238	AX214238 Sequence
5	15	100.0	28	6	AX214240	AX214240 Sequence
6	15	100.0	28	6	AX214241	AX214241 Sequence
7	15	100.0	28	6	AX214242	AX214242 Sequence
8	15	100.0	28	6	AX214243	AX214243 Sequence
9	15	100.0	28	6	AX214244	AX214244 Sequence
10	15	100.0	28	6	AX214245	AX214245 Sequence
11	15	100.0	28	6	AX214246	AX214246 Sequence
12	15	100.0	28	6	AX214247	AX214247 Sequence
13	15	100.0	28	6	AX214248	AX214248 Sequence
14	15	100.0	28	6	AX214249	AX214249 Sequence
15	15	100.0	28	6	AX214250	AX214250 Sequence
16	15	100.0	28	6	AX214251	AX214251 Sequence
17	15	100.0	28	6	AX214252	AX214252 Sequence
18	15	100.0	28	6	AX214253	AX214253 Sequence
19	15	100.0	28	6	AX214254	AX214254 Sequence
20	15	100.0	28	6	AX214255	AX214255 Sequence
21	15	100.0	28	6	AX214256	AX214256 Sequence
22	15	100.0	28	6	AX214257	AX214257 Sequence
23	15	100.0	28	6	AX214258	AX214258 Sequence
24	15	100.0	28	6	AX214259	AX214259 Sequence
25	15	100.0	28	6	AX214260	AX214260 Sequence
26	15	100.0	28	6	AX214261	AX214261 Sequence
27	15	100.0	28	6	AX214262	AX214262 Sequence
28	15	100.0	28	6	AX214263	AX214263 Sequence
29	15	100.0	28	6	AX214264	AX214264 Sequence
30	15	100.0	28	6	AX214265	AX214265 Sequence
31	15	100.0	28	6	AX214266	AX214266 Sequence
32	15	100.0	28	6	AX214267	AX214267 Sequence
33	15	100.0	28	6	AX214268	AX214268 Sequence
34	15	100.0	28	6	AX214269	AX214269 Sequence
35	15	100.0	28	6	AX214270	AX214270 Sequence
36	15	100.0	28	6	AX214271	AX214271 Sequence
37	15	100.0	28	6	AX214272	AX214272 Sequence
38	15	100.0	28	6	AX214273	AX214273 Sequence
39	15	100.0	28	6	AX214274	AX214274 Sequence
40	15	100.0	28	6	AX214275	AX214275 Sequence
41	15	100.0	28	6	AX214276	AX214276 Sequence
42	15	100.0	28	6	AX214277	AX214277 Sequence
43	15	100.0	28	6	AX214278	AX214278 Sequence
44	15	100.0	28	6	AX214279	AX214279 Sequence
45	15	100.0	28	6	AX214280	AX214280 Sequence

ALIGNMENTS

RESULT 1
AX214295
LOCUS AX214295 15 bp mRNA linear PAT 06-SEP-2001
DEFINITION Sequence 108 from Patent WO0159102.
ACCESSION AX214295
VERSION AX214295.1 GI:15524372
KEYWORDS .
SOURCE synthetic construct.
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 15)
AUTHORS Breaker,R. and Emilsson,G.
TITLE Nucleozymes with endonuclease activity
JOURNAL Patent: WO 0159102-A 108 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; Yale University (US)

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FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="Nucleic Acid"
BASE COUNT        7 a      1 c      4 g      3 t
ORIGIN

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  Best Local Similarity   80.0%;  Pred. No. 9.9e+02;
  Matches   12;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAUAACGUGAAGAU 15
              |||:||||:|||||:
Db          1 AGATAACGTGAAGAT 15


RESULT 2
AX214239
LOCUS       AX214239                  27 bp    mRNA    linear   PAT 06-SEP-2001
DEFINITION  Sequence 52 from Patent WO0159102.
ACCESSION   AX214239
VERSION     AX214239.1  GI:15524316
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 27)
  AUTHORS   Breaker,R. and Emilsson,G.
  TITLE     Nucleozymes with endonuclease activity
  JOURNAL   Patent: WO 0159102-A 52 16-AUG-2001;
            RIBOZYME PHARMACEUTICALS, INC. (US) ; Yale University (US)
FEATURES             Location/Qualifiers
     source          1. .27
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="Nucleic Acid"
BASE COUNT       11 a      3 c      9 g      4 t
ORIGIN

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  Best Local Similarity   80.0%;  Pred. No. 9.4e+02;
  Matches   12;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAUAACGUGAAGAU 15
              |||:||||:|||||:
Db          7 AGATAACGTGAAGAT 21


RESULT 3
AX214237
LOCUS       AX214237                  28 bp    mRNA    linear   PAT 06-SEP-2001
DEFINITION  Sequence 50 from Patent WO0159102.
ACCESSION   AX214237
VERSION     AX214237.1  GI:15524314
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 28)
  AUTHORS   Breaker,R. and Emilsson,G.
  TITLE     Nucleozymes with endonuclease activity
  JOURNAL   Patent: WO 0159102-A 50 16-AUG-2001;
            RIBOZYME PHARMACEUTICALS, INC. (US) ; Yale University (US)
FEATURES             Location/Qualifiers
     source          1. .28
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="Nucleic Acid"
     misc_feature    1. .6
                     /note="2'-O-Methyl"
     misc_feature    21. .27
                     /note="2'-O-Methyl"
     misc_feature    28
                     /note="n stands for inverted deoxyabasic derivative"
BASE COUNT       11 a      3 c      9 g      4 t      1 others
ORIGIN

  Query Match             100.0%;  Score 15;  DB 6;  Length 28;
  Best Local Similarity   80.0%;  Pred. No. 9.3e+02;
  Matches   12;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAUAACGUGAAGAU 15
              |||:||||:|||||:
Db          7 AGATAACGTGAAGAT 21


RESULT 4
AX214238
LOCUS       AX214238                  28 bp    mRNA    linear   PAT 06-SEP-2001
DEFINITION  Sequence 51 from Patent WO0159102.
ACCESSION   AX214238
VERSION     AX214238.1  GI:15524315
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 28)
  AUTHORS   Breaker,R. and Emilsson,G.
  TITLE     Nucleozymes with endonuclease activity
  JOURNAL   Patent: WO 0159102-A 51 16-AUG-2001;
            RIBOZYME PHARMACEUTICALS, INC. (US) ; Yale University (US)
FEATURES             Location/Qualifiers
     source          1. .28
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="Nucleic Acid"
     misc_feature    1. .5
                     /note="2'-O-Methyl"
     misc_feature    21. .27
                     /note="2'-O-Methyl"
     misc_feature    28
                     /note="n stands for inverted deoxyabasic derivative"
BASE COUNT       11 a      3 c      9 g      4 t      1 others
ORIGIN

  Query Match             100.0%;  Score 15;  DB 6;  Length 28;
  Best Local Similarity   80.0%;  Pred. No. 9.3e+02;
  Matches   12;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAUAACGUGAAGAU 15
              |||:||||:|||||:
Db          7 AGATAACGTGAAGAT 21


RESULT 5
AX214240
LOCUS       AX214240                  28 bp    mRNA    linear   PAT 06-SEP-2001
DEFINITION  Sequence 53 from Patent WO0159102.
ACCESSION   AX214240
VERSION     AX214240.1  GI:15524317
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 28)
  AUTHORS   Breaker,R. and Emilsson,G.
  TITLE     Nucleozymes with endonuclease activity
  JOURNAL   Patent: WO 0159102-A 53 16-AUG-2001;
            RIBOZYME PHARMACEUTICALS, INC. (US) ; Yale University (US)
FEATURES             Location/Qualifiers
     source          1. .28
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="Nucleic Acid"
     misc_feature    1. .5
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                     /note="2'-O-Methyl"
     misc_feature    22. .27
                     /note="2'-O-Methyl"
     misc_feature    28
                     /note="n stands for inverted deoxyabasic derivative"
BASE COUNT       11 a      3 c      9 g      4 t      1 others
ORIGIN

  Query Match             100.0%;  Score 15;  DB 6;  Length 28;
  Best Local Similarity   80.0%;  Pred. No. 9.3e+02;
  Matches   12;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAUAACGUGAAGAU 15
              |||:||||:|||||:
Db          7 AGATAACGTGAAGAT 21


RESULT 6
AX214241
LOCUS       AX214241                 28 bp    mRNA    linear   PAT 06-SEP-2001
DEFINITION  Sequence 54 from Patent WO0159102.
ACCESSION   AX214241
VERSION     AX214241.1  GI:15524318
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 28)
  AUTHORS   Breaker,R. and Emilsson,G.
  TITLE     Nucleozymes with endonuclease activity
  JOURNAL   Patent: WO 0159102-A 54 16-AUG-2001;
            RIBOZYME PHARMACEUTICALS, INC. (US) ; Yale University (US)
FEATURES             Location/Qualifiers
     source          1. .28
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="Nucleic Acid"
     misc_feature    1. .5
                     /note="2'-O-Methyl"
     misc_feature    23. .27
                     /note="2'-O-Methyl"
     misc_feature    28
                     /note="n stands for inverted deoxyabasic derivative"
BASE COUNT       11 a      3 c      9 g      4 t      1 others
ORIGIN

  Query Match             100.0%;  Score 15;  DB 6;  Length 28;
  Best Local Similarity   80.0%;  Pred. No. 9.3e+02;
  Matches   12;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAUAACGUGAAGAU 15
              |||:||||:|||||:
Db          7 AGATAACGTGAAGAT 21


RESULT 7
AX214242
LOCUS       AX214242                 28 bp    mRNA    linear   PAT 06-SEP-2001
DEFINITION  Sequence 55 from Patent WO0159102.
ACCESSION   AX214242
VERSION     AX214242.1  GI:15524319
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 28)
  AUTHORS   Breaker,R. and Emilsson,G.
  TITLE     Nucleozymes with endonuclease activity
  JOURNAL   Patent: WO 0159102-A 55 16-AUG-2001;
            RIBOZYME PHARMACEUTICALS, INC. (US) ; Yale University (US)
FEATURES             Location/Qualifiers
     source          1. .28
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="Nucleic Acid"
     misc_feature    1. .4
                     /note="2'-O-Methyl"
     misc_feature    24. .27
                     /note="2'-O-Methyl"
     misc_feature    28
                     /note="n stands for inverted deoxyabasic derivative"
BASE COUNT       11 a      3 c      9 g      4 t      1 others
ORIGIN

  Query Match             100.0%;  Score 15;  DB 6;  Length 28;
  Best Local Similarity   80.0%;  Pred. No. 9.3e+02;
  Matches   12;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAUAACGUGAAGAU 15
              |||:||||:|||||:
Db          7 AGATAACGTGAAGAT 21


RESULT 8
AX214243
LOCUS       AX214243                 28 bp    mRNA    linear   PAT 06-SEP-2001
DEFINITION  Sequence 56 from Patent WO0159102.
ACCESSION   AX214243
VERSION     AX214243.1  GI:15524320
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 28)
  AUTHORS   Breaker,R. and Emilsson,G.
  TITLE     Nucleozymes with endonuclease activity
  JOURNAL   Patent: WO 0159102-A 56 16-AUG-2001;
            RIBOZYME PHARMACEUTICALS, INC. (US) ; Yale University (US)
FEATURES             Location/Qualifiers
     source          1. .28
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="Nucleic Acid"
     misc_feature    1. .4
                     /note="2'-O-Methyl"
     misc_feature    23. .27
                     /note="2'-O-Methyl"
     misc_feature    28
                     /note="n stands for inverted deoxyabasic derivative"
BASE COUNT       11 a      3 c      9 g      4 t      1 others
ORIGIN

  Query Match             100.0%;  Score 15;  DB 6;  Length 28;
  Best Local Similarity   80.0%;  Pred. No. 9.3e+02;
  Matches   12;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAUAACGUGAAGAU 15
              |||:||||:|||||:
Db          7 AGATAACGTGAAGAT 21


RESULT 9
AX214244
LOCUS       AX214244                 28 bp    mRNA    linear   PAT 06-SEP-2001
DEFINITION  Sequence 57 from Patent WO0159102.
ACCESSION   AX214244
VERSION     AX214244.1  GI:15524321
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 28)
  AUTHORS   Breaker,R. and Emilsson,G.
  TITLE     Nucleozymes with endonuclease activity
  JOURNAL   Patent: WO 0159102-A 57 16-AUG-2001;
            RIBOZYME PHARMACEUTICALS, INC. (US) ; Yale University (US)
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FEATURES             Location/Qualifiers
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                     /db_xref="taxon:32630"
                     /note="Nucleic Acid"
     misc_feature    1. .6
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     misc_feature    20. .27
                     /note="2'-O-Methyl"
     misc_feature    28
                     /note="n stands for inverted deoxyabasic derivative"
BASE COUNT       11 a      3 c      9 g      4 t      1 others
ORIGIN

  Query Match             100.0%;  Score 15;  DB 6;  Length 28;
  Best Local Similarity   80.0%;  Pred. No. 9.3e+02;
  Matches   12;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAUAACGUGAAGAU 15
              |||:||||:|||||:
Db          7 AGATAACGTGAAGAT 21


RESULT 10
AX214245
LOCUS       AX214245                  28 bp    mRNA    linear   PAT 06-SEP-2001
DEFINITION  Sequence 58 from Patent WO0159102.
ACCESSION   AX214245
VERSION     AX214245.1  GI:15524322
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 28)
  AUTHORS   Breaker,R. and Emilsson,G.
  TITLE     Nucleozymes with endonuclease activity
  JOURNAL   Patent: WO 0159102-A 58 16-AUG-2001;
            RIBOZYME PHARMACEUTICALS, INC. (US) ; Yale University (US)
FEATURES             Location/Qualifiers
     source          1. .28
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="Nucleic Acid"
     misc_feature    1. .6
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     misc_feature    12
                     /note="2'-O-Methyl"
     misc_feature    21. .27
                     /note="2'-O-Methyl"
     misc_feature    28
                     /note="n stands for inverted deoxyabasic derivative"
BASE COUNT       11 a      3 c      9 g      4 t      1 others
ORIGIN

  Query Match             100.0%;  Score 15;  DB 6;  Length 28;
  Best Local Similarity   80.0%;  Pred. No. 9.3e+02;
  Matches   12;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAUAACGUGAAGAU 15
              |||:||||:|||||:
Db          7 AGATAACGTGAAGAT 21


RESULT 11
AX214246
LOCUS       AX214246                  28 bp    mRNA    linear   PAT 06-SEP-2001
DEFINITION  Sequence 59 from Patent WO0159102.
ACCESSION   AX214246
VERSION     AX214246.1  GI:15524323
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences..
REFERENCE   1  (bases 1 to 28)
  AUTHORS   Breaker,R. and Emilsson,G.
  TITLE     Nucleozymes with endonuclease activity
  JOURNAL   Patent: WO 0159102-A 59 16-AUG-2001;
            RIBOZYME PHARMACEUTICALS, INC. (US) ; Yale University (US)
FEATURES             Location/Qualifiers
     source          1. .28
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="Nucleic Acid"
     misc_feature    1. .7
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     misc_feature    21. .27
                     /note="2'-O-Methyl"
     misc_feature    28
                     /note="n stands for inverted deoxyabasic derivative"
BASE COUNT       11 a      3 c      9 g      4 t      1 others
ORIGIN

  Query Match             100.0%;  Score 15;  DB 6;  Length 28;
  Best Local Similarity   80.0%;  Pred. No. 9.3e+02;
  Matches   12;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAUAACGUGAAGAU 15
              |||:||||:|||||:
Db          7 AGATAACGTGAAGAT 21


RESULT 12
AX214247
LOCUS       AX214247                  28 bp    mRNA    linear   PAT 06-SEP-2001
DEFINITION  Sequence 60 from Patent WO0159102.
ACCESSION   AX214247
VERSION     AX214247.1  GI:15524324
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 28)
  AUTHORS   Breaker,R. and Emilsson,G.
  TITLE     Nucleozymes with endonuclease activity
  JOURNAL   Patent: WO 0159102-A 60 16-AUG-2001;
            RIBOZYME PHARMACEUTICALS, INC. (US) ; Yale University (US)
FEATURES             Location/Qualifiers
     source          1. .28
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="Nucleic Acid"
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     misc_feature    21. .27
                     /note="2'-O-Methyl"
     misc_feature    28
                     /note="n stands for inverted deoxyabasic derivative"
BASE COUNT       11 a      3 c      9 g      4 t      1 others
ORIGIN

  Query Match             100.0%;  Score 15;  DB 6;  Length 28;
  Best Local Similarity   80.0%;  Pred. No. 9.3e+02;
  Matches   12;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAUAACGUGAAGAU 15
              |||:||||:|||||:
Db          7 AGATAACGTGAAGAT 21


RESULT 13
AX214248
LOCUS       AX214248                  28 bp    mRNA    linear   PAT 06-SEP-2001
DEFINITION  Sequence 61 from Patent WO0159102.
ACCESSION   AX214248
VERSION     AX214248  GI:15524325
KEYWORDS    .
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SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 28)
  AUTHORS   Breaker,R. and Emilsson,G.
  TITLE     Nucleozymes with endonuclease activity
  JOURNAL   Patent: WO 0159102-A 61 16-AUG-2001;
            RIBOZYME PHARMACEUTICALS, INC. (US) ; Yale University (US)
FEATURES             Location/Qualifiers
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                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="Nucleic Acid"
     misc_feature    1. .6
                     /note="2'-O-Methyl"
     misc_feature    18
                     /note="2'-O-Methyl"
     misc_feature    21. .27
                     /note="2'-O-Methyl"
     misc_feature    28
                     /note="n stands for inverted deoxyabasic derivative"
BASE COUNT       11 a      3 c      9 g      4 t      1 others
ORIGIN

  Query Match             100.0%;  Score 15;  DB 6;  Length 28;
  Best Local Similarity   80.0%;  Pred. No. 9.3e+02;
  Matches   12;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAUAACGUGAAGAU 15
              |||:||||:|||||:
Db          7 AGATAACGTGAAGAT 21


RESULT 14
AX214249
LOCUS       AX214249                  28 bp    mRNA    linear   PAT 06-SEP-2001
DEFINITION  Sequence 62 from Patent WO0159102.
ACCESSION   AX214249
VERSION     AX214249.1  GI:15524326
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 28)
  AUTHORS   Breaker,R. and Emilsson,G.
  TITLE     Nucleozymes with endonuclease activity
  JOURNAL   Patent: WO 0159102-A 62 16-AUG-2001;
            RIBOZYME PHARMACEUTICALS, INC. (US) ; Yale University (US)
FEATURES             Location/Qualifiers
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                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="Nucleic Acid"
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     misc_feature    21. .27
                     /note="2'-O-Methyl"
     misc_feature    28
                     /note="n stands for inverted deoxyabasic derivative"
BASE COUNT       11 a      3 c      9 g      4 t      1 others
ORIGIN

  Query Match             100.0%;  Score 15;  DB 6;  Length 28;
  Best Local Similarity   80.0%;  Pred. No. 9.3e+02;
  Matches   12;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAUAACGUGAAGAU 15
              |||:||||:|||||:
Db          7 AGATAACGTGAAGAT 21


RESULT 15
AX214250
LOCUS       AX214250                  28 bp    mRNA    linear   PAT 06-SEP-2001
DEFINITION  Sequence 63 from Patent WO0159102.
ACCESSION   AX214250
VERSION     AX214250.1  GI:15524327
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 28)
  AUTHORS   Breaker,R. and Emilsson,G.
  TITLE     Nucleozymes with endonuclease activity
  JOURNAL   Patent: WO 0159102-A 63 16-AUG-2001;
            RIBOZYME PHARMACEUTICALS, INC. (US) ; Yale University (US)
FEATURES             Location/Qualifiers
     source          1. .28
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="Nucleic Acid"
     misc_feature    1. .6
                     /note="2'-O-Methyl"
     misc_feature    11
                     /note="2'-O-Methyl"
     misc_feature    16
                     /note="2'-O-Methyl"
     misc_feature    21. .27
                     /note="2'-O-Methyl"
     misc_feature    28
                     /note="n stands for inverted deoxyabasic derivative"
BASE COUNT       11 a      3 c      9 g      4 t      1 others
ORIGIN

  Query Match             100.0%;  Score 15;  DB 6;  Length 28;
  Best Local Similarity   80.0%;  Pred. No. 9.3e+02;
  Matches   12;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAUAACGUGAAGAU 15
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Db          7 AGATAACGTGAAGAT 21


Search completed: July  6, 2003, 14:51:11
Job time : 493.182 secs
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: July 6, 2003, 14:25:15 ; Search time 160.909 Seconds
(without alignments)
209.932 Million cell updates/sec

Title: US-09-780-929-97
Perfect score: 15
Sequence: 1 agauaacgugaagau 15

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 2274872

Minimum DB seq length: 0
Maximum DB seq length: 60

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	15	100.0	15	22	AAS12347	DNA encoding deoxy
2	15	100.0	27	22	AAS12295	DNA encoding class
3	15	100.0	27	22	AAS12296	DNA encoding class
4	15	100.0	27	22	AAS12297	DNA encoding class
5	15	100.0	27	22	AAS12298	DNA encoding class
6	15	100.0	27	22	AAS12299	DNA encoding class
7	15	100.0	27	22	AAS12300	DNA encoding class
8	15	100.0	27	22	AAS12301	DNA encoding class
9	15	100.0	27	22	AAS12302	DNA encoding class
10	15	100.0	27	22	AAS12303	DNA encoding class
11	15	100.0	27	22	AAS12304	DNA encoding class
12	15	100.0	27	22	AAS12305	DNA encoding class
13	15	100.0	27	22	AAS12306	DNA encoding class
14	15	100.0	27	22	AAS12307	DNA encoding class
15	15	100.0	27	22	AAS12308	DNA encoding class
16	15	100.0	27	22	AAS12309	DNA encoding class
17	15	100.0	27	22	AAS12310	DNA encoding class
18	15	100.0	27	22	AAS12311	DNA encoding class
19	15	100.0	27	22	AAS12312	DNA encoding class
20	15	100.0	27	22	AAS12313	DNA encoding class
21	15	100.0	27	22	AAS12314	DNA encoding class
22	15	100.0	27	22	AAS12315	DNA encoding class
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24	15	100.0	27	22	AAS12317	DNA encoding class
25	15	100.0	27	22	AAS12318	DNA encoding class
26	15	100.0	27	22	AAS12319	DNA encoding class
27	15	100.0	27	22	AAS12320	DNA encoding class
28	15	100.0	27	22	AAS12321	DNA encoding class
29	15	100.0	27	22	AAS12322	DNA encoding class
30	15	100.0	27	22	AAS12323	DNA encoding class
31	15	100.0	27	22	AAS12324	DNA encoding class
32	15	100.0	27	22	AAS12325	DNA encoding class
33	15	100.0	27	22	AAS12326	DNA encoding class
34	15	100.0	27	22	AAS12327	DNA encoding class
35	15	100.0	27	22	AAS12328	DNA encoding class
36	15	100.0	27	22	AAS12329	DNA encoding class
37	15	100.0	27	22	AAS12330	DNA encoding class
38	15	100.0	27	22	AAS12331	DNA encoding class
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40	15	100.0	27	22	AAS12333	DNA encoding class
41	15	100.0	27	22	AAS12334	DNA encoding class
42	15	100.0	27	22	AAS12335	DNA encoding class
43	15	100.0	27	22	AAS12336	DNA encoding class
44	15	100.0	27	22	AAS12337	DNA encoding class
45	15	100.0	27	22	AAS12404	DNA encoding class

ALIGNMENTS

RESULT 1
AAS12347
ID AAS12347 standard; DNA; 15 BP.
XX
AC AAS12347;
XX
DT 21-NOV-2001 (first entry)
XX
DE DNA encoding deoxyribozyme #7.
XX
KW Deoxyribozyme; cytostatic; endonuclease; RNA cleavage; DNA cleavage;
KW gene therapy; plant; fungus; bacteria; mammal; ribozyme; ss.
XX
OS Synthetic.
XX
PN WO200159102-A2.
XX
PD 16-AUG-2001.
XX
PF 08-FEB-2001; 2001WO-US04223.
XX
PR 08-FEB-2000; 2000US-0181360.
PR 31-MAR-2000; 2000US-0193646.
XX
PA (RIBO-) RIBOZYME PHARM INC.
PA (UYYA) UNIV YALE.
XX
PI Breaker R, Beigelman L, Emilsson G;
XX
DR WPI; 2001-536526/59.
XX
PT New nucleic acids with endonuclease activity, such as ribozymes and

```
PT   nucleozymes, for modulating gene expression in a plant, mammalian,
PT   bacterial or fungal cell  -
XX
PS   Claim 49; Page 77; 96pp; English.
XX
CC   The invention relates to nucleic acid molecules with endonuclease
CC   activity, which are particularly useful for cleavage of RNA or DNA.
CC   The nucleic acids are used in a pharmaceutical composition and are used
CC   to modulate expression of a gene in a plant, mammalian, bacterial or
CC   fungal cell. They are used to cleave a separate nucleic acid, preferably
CC   RNA. The nucleic acids are used to inhibit gene expression and/or cell
CC   proliferation, and can be used to treat a disease or condition. More
CC   than one nucleic acid can be independently targeted to the same or
CC   different sites in a cell. The nucleic acids may be used to study DNA.
CC   The modifications to the nucleic acids optimises their catalytic activity
CC   and can maintain or enhance their activity. They exhibit a high degree
CC   of specificity for RNA. The present sequence represents the coding
CC   sequence of deoxyribozyme #7 used in the method of the invention.
XX
SQ   Sequence 15 BP; 7 A; 1 C; 4 G; 3 U; 0 other;

  Query Match           100.0%;  Score 15;  DB 22;  Length 15;
  Best Local Similarity  100.0%;  Pred. No. 71;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAUAACGUGAAGAU 15
              ||||||||||||||||
Db          1 AGAUAACGUGAAGAU 15


RESULT 2
AAS12295
ID   AAS12295 standard; DNA; 27 BP.
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AC   AAS12295;
XX
DT   21-NOV-2001  (first entry)
XX
DE   DNA encoding class V ribozyme #7.
XX
KW   Ribozyme; cytostatic; endonuclease; RNA cleavage; DNA cleavage;
KW   gene therapy; plant; fungus; bacteria; mammal; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1..4
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "OTHER = 2'-O-methyl nucleotides"
FT   modified_base   23..27
FT                   /*tag=  b
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FT                   /note= "OTHER = 2'-O-methyl nucleotides"
FT   modified_base   27
FT                   /*tag=  c
FT                   /mod_base= c
FT                   /note= "3',3'-inverted deoxyabasic moiety"
XX
PN   WO200159102-A2.
XX
PD   16-AUG-2001.
XX
PF   08-FEB-2001; 2001WO-US04223.
XX
PR   08-FEB-2000; 2000US-0181360.
PR   31-MAR-2000; 2000US-0193646.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
PA   (UYYA ) UNIV YALE.
XX
PI   Breaker R,  Beigelman L,  Emilsson G;
XX
DR   WPI; 2001-536526/59.
XX
PT   New nucleic acids with endonuclease activity, such as ribozymes and
PT   nucleozymes, for modulating gene expression in a plant, mammalian,
PT   bacterial or fungal cell  -
XX
PS   Example 1; Page 71; 96pp; English.
XX
CC   The invention relates to nucleic acid molecules with endonuclease
CC   activity, which are particularly useful for cleavage of RNA or DNA.
CC   The nucleic acids are used in a pharmaceutical composition and are used
CC   to modulate expression of a gene in a plant, mammalian, bacterial or
CC   fungal cell. They are used to cleave a separate nucleic acid, preferably
CC   RNA. The nucleic acids are used to inhibit gene expression and/or cell
CC   proliferation, and can be used to treat a disease or condition. More
CC   than one nucleic acid can be independently targeted to the same or
CC   different sites in a cell. The nucleic acids may be used to study DNA.
CC   The modifications to the nucleic acids optimises their catalytic activity
CC   and can maintain or enhance their activity. They exhibit a high degree
CC   of specificity for RNA. The present sequence represents the coding
CC   sequence of class V ribozyme #7 used in the method of the invention.
XX
SQ   Sequence 27 BP; 11 A; 3 C; 9 G; 4 U; 0 other;

  Query Match           100.0%;  Score 15;  DB 22;  Length 27;
  Best Local Similarity  100.0%;  Pred. No. 74;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAUAACGUGAAGAU 15
              ||||||||||||||||
Db          7 AGAUAACGUGAAGAU 21


RESULT 3
AAS12296
ID   AAS12296 standard; DNA; 27 BP.
XX
AC   AAS12296;
XX
DT   21-NOV-2001  (first entry)
XX
DE   DNA encoding class V ribozyme #8.
XX
KW   Ribozyme; cytostatic; endonuclease; RNA cleavage; DNA cleavage;
KW   gene therapy; plant; fungus; bacteria; mammal; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1..6
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "OTHER = 2'-O-methyl nucleotides"
FT   modified_base   20..27
FT                   /*tag=  b
FT                   /mod_base= OTHER
FT                   /note= "OTHER = 2'-O-methyl nucleotides"
FT   modified_base   27
FT                   /*tag=  c
FT                   /mod_base= c
FT                   /note= "3',3'-inverted deoxyabasic moiety"
XX
PN   WO200159102-A2.
XX
PD   16-AUG-2001.
XX
PF   08-FEB-2001; 2001WO-US04223.
XX
PR   08-FEB-2000; 2000US-0181360.
PR   31-MAR-2000; 2000US-0193646.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
PA   (UYYA ) UNIV YALE.
```

```
XX
PI   Breaker R,  Beigelman L,  Emilsson G;
XX
DR   WPI; 2001-536526/59.
XX
PT   New nucleic acids with endonuclease activity, such as ribozymes and
PT   nucleozymes, for modulating gene expression in a plant, mammalian,
PT   bacterial or fungal cell  -
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PS   Example 1; Page 71; 96pp; English.
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CC   activity, which are particularly useful for cleavage of RNA or DNA.
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CC   fungal cell. They are used to cleave a separate nucleic acid, preferably
CC   RNA. The nucleic acids are used to inhibit gene expression and/or cell
CC   proliferation, and can be used to treat a disease or condition. More
CC   than one nucleic acid can be independently targeted to the same or
CC   different sites in a cell. The nucleic acids may be used to study DNA.
CC   The modifications to the nucleic acids optimises their catalytic activity
CC   and can maintain or enhance their activity. They exhibit a high degree
CC   of specificity for RNA. The present sequence represents the coding
CC   sequence of class V ribozyme #8 used in the method of the invention.
XX
SQ   Sequence 27 BP; 11 A; 3 C; 9 G; 4 U; 0 other;

  Query Match             100.0%;  Score 15;  DB 22;  Length 27;
  Best Local Similarity   100.0%;  Pred. No. 74;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAUAACGUGAAGAU 15
              |||||||||||||||
Db          7 AGAUAACGUGAAGAU 21


RESULT 4
AAS12297
ID   AAS12297 standard; DNA; 27 BP.
XX
AC   AAS12297;
XX
DT   21-NOV-2001  (first entry)
XX
DE   DNA encoding class V ribozyme #9.
XX
KW   Ribozyme; cytostatic; endonuclease; RNA cleavage; DNA cleavage;
KW   gene therapy; plant; fungus; bacteria; mammal; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1..6
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "OTHER = 2'-O-methyl nucleotides"
FT   modified_base   21..27
FT                   /*tag=  b
FT                   /mod_base= OTHER
FT                   /note= "OTHER = 2'-O-methyl nucleotides"
FT   modified_base   27
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FT                   /note= "3',3'-inverted deoxyabasic moiety"
XX
PN   WO200159102-A2.
XX
PD   16-AUG-2001.
XX
PF   08-FEB-2001; 2001WO-US04223.
XX
PR   08-FEB-2000; 2000US-0181360.
PR   31-MAR-2000; 2000US-0193646.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
PA   (UYYA ) UNIV YALE.
XX
PI   Breaker R,  Beigelman L,  Emilsson G;
XX
DR   WPI; 2001-536526/59.
XX
PT   New nucleic acids with endonuclease activity, such as ribozymes and
PT   nucleozymes, for modulating gene expression in a plant, mammalian,
PT   bacterial or fungal cell  -
XX
PS   Example 1; Page 71; 96pp; English.
XX
CC   The invention relates to nucleic acid molecules with endonuclease
CC   activity, which are particularly useful for cleavage of RNA or DNA.
CC   The nucleic acids are used in a pharmaceutical composition and are used
CC   to modulate expression of a gene in a plant, mammalian, bacterial or
CC   fungal cell. They are used to cleave a separate nucleic acid, preferably
CC   RNA. The nucleic acids are used to inhibit gene expression and/or cell
CC   proliferation, and can be used to treat a disease or condition. More
CC   than one nucleic acid can be independently targeted to the same or
CC   different sites in a cell. The nucleic acids may be used to study DNA.
CC   The modifications to the nucleic acids optimises their catalytic activity
CC   and can maintain or enhance their activity. They exhibit a high degree
CC   of specificity for RNA. The present sequence represents the coding
CC   sequence of class V ribozyme #9 used in the method of the invention.
XX
SQ   Sequence 27 BP; 11 A; 3 C; 9 G; 4 U; 0 other;

  Query Match             100.0%;  Score 15;  DB 22;  Length 27;
  Best Local Similarity   100.0%;  Pred. No. 74;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAUAACGUGAAGAU 15
              |||||||||||||||
Db          7 AGAUAACGUGAAGAU 21


RESULT 5
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ID   AAS12298 standard; DNA; 27 BP.
XX
AC   AAS12298;
XX
DT   21-NOV-2001  (first entry)
XX
DE   DNA encoding class V ribozyme #10.
XX
KW   Ribozyme; cytostatic; endonuclease; RNA cleavage; DNA cleavage;
KW   gene therapy; plant; fungus; bacteria; mammal; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1..6
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "OTHER = 2'-O-methyl nucleotides"
FT   modified_base   12
FT                   /*tag=  b
FT                   /mod_base= OTHER
FT                   /note= "OTHER = 2'-O-methyl nucleotide"
FT   modified_base   21..27
FT                   /*tag=  c
FT                   /mod_base= OTHER
FT                   /note= "OTHER = 2'-O-methyl nucleotides"
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FT                   /mod_base= c
FT                   /note= "3',3'-inverted deoxyabasic moiety"
XX
PN   WO200159102-A2.
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XX
PD   16-AUG-2001.
XX
PF   08-FEB-2001; 2001WO-US04223.
XX
PR   08-FEB-2000; 2000US-0181360.
PR   31-MAR-2000; 2000US-0193646.
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PA   (UYYA ) UNIV YALE.
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PI   Breaker R,  Beigelman L,  Emilsson G;
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DR   WPI; 2001-536526/59.
XX
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PT   nucleozymes, for modulating gene expression in a plant, mammalian,
PT   bacterial or fungal cell  -
XX
PS   Example 1; Page 71; 96pp; English.
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CC   The invention relates to nucleic acid molecules with endonuclease
CC   activity, which are particularly useful for cleavage of RNA or DNA.
CC   The nucleic acids are used in a pharmaceutical composition and are used
CC   to modulate expression of a gene in a plant, mammalian, bacterial or
CC   fungal cell. They are used to cleave a separate nucleic acid, preferably
CC   RNA. The nucleic acids are used to inhibit gene expression and/or cell
CC   proliferation, and can be used to treat a disease or condition. More
CC   than one nucleic acid can be independently targeted to the same or
CC   different sites in a cell. The nucleic acids may be used to study DNA.
CC   The modifications to the nucleic acids optimises their catalytic activity
CC   and can maintain or enhance their activity. They exhibit a high degree
CC   of specificity for RNA. The present sequence represents the coding
CC   sequence of class V ribozyme #10 used in the method of the invention.
XX
SQ   Sequence 27 BP; 11 A; 3 C; 9 G; 4 U; 0 other;

  Query Match             100.0%;  Score 15;  DB 22;  Length 27;
  Best Local Similarity   100.0%;  Pred. No. 74;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAUAACGUGAAGAU 15
              |||||||||||||||
Db          7 AGAUAACGUGAAGAU 21


RESULT 6
AAS12299
ID   AAS12299 standard; DNA; 27 BP.
XX
AC   AAS12299;
XX
DT   21-NOV-2001  (first entry)
XX
DE   DNA encoding class V ribozyme #11.
XX
KW   Ribozyme; cytostatic; endonuclease; RNA cleavage; DNA cleavage;
KW   gene therapy; plant; fungus; bacteria; mammal; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1..7
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "OTHER = 2'-O-methyl nucleotides"
FT   modified_base   21..27
FT                   /*tag=  b
FT                   /mod_base= OTHER
FT                   /note= "OTHER = 2'-O-methyl nucleotides"
FT   modified_base   27
FT                   /*tag=  c
FT                   /mod_base= c
FT                   /note= "3',3'-inverted deoxyabasic moiety"
XX
PN   WO200159102-A2.
XX
PD   16-AUG-2001.
XX
PF   08-FEB-2001; 2001WO-US04223.
XX
PR   08-FEB-2000; 2000US-0181360.
PR   31-MAR-2000; 2000US-0193646.
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PA   (RIBO-) RIBOZYME PHARM INC.
PA   (UYYA ) UNIV YALE.
XX
PI   Breaker R,  Beigelman L,  Emilsson G;
XX
DR   WPI; 2001-536526/59.
XX
PT   New nucleic acids with endonuclease activity, such as ribozymes and
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XX
PS   Example 1; Page 71; 96pp; English.
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CC   fungal cell. They are used to cleave a separate nucleic acid, preferably
CC   RNA. The nucleic acids are used to inhibit gene expression and/or cell
CC   proliferation, and can be used to treat a disease or condition. More
CC   than one nucleic acid can be independently targeted to the same or
CC   different sites in a cell. The nucleic acids may be used to study DNA.
CC   The modifications to the nucleic acids optimises their catalytic activity
CC   and can maintain or enhance their activity. They exhibit a high degree
CC   of specificity for RNA. The present sequence represents the coding
CC   sequence of class V ribozyme #11 used in the method of the invention.
XX
SQ   Sequence 27 BP; 11 A; 3 C; 9 G; 4 U; 0 other;

  Query Match             100.0%;  Score 15;  DB 22;  Length 27;
  Best Local Similarity   100.0%;  Pred. No. 74;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAUAACGUGAAGAU 15
              |||||||||||||||
Db          7 AGAUAACGUGAAGAU 21


RESULT 7
AAS12300
ID   AAS12300 standard; DNA; 27 BP.
XX
AC   AAS12300;
XX
DT   21-NOV-2001  (first entry)
XX
DE   DNA encoding class V ribozyme #12.
XX
KW   Ribozyme; cytostatic; endonuclease; RNA cleavage; DNA cleavage;
KW   gene therapy; plant; fungus; bacteria; mammal; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1..6
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "OTHER = 2'-O-methyl nucleotides"
FT   modified_base   21..27
FT                   /*tag=  b
FT                   /mod_base= OTHER
FT                   /note= "OTHER = 2'-O-methyl nucleotides"
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FT   modified_base   27
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XX
PN   WO200159102-A2.
XX
PD   16-AUG-2001.
XX
PF   08-FEB-2001; 2001WO-US04223.
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PR   08-FEB-2000; 2000US-0181360.
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PT   New nucleic acids with endonuclease activity, such as ribozymes and
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CC   RNA. The nucleic acids are used to inhibit gene expression and/or cell
CC   proliferation, and can be used to treat a disease or condition. More
CC   than one nucleic acid can be independently targeted to the same or
CC   different sites in a cell. The nucleic acids may be used to study DNA.
CC   The modifications to the nucleic acids optimises their catalytic activity
CC   and can maintain or enhance their activity. They exhibit a high degree
CC   of specificity for RNA. The present sequence represents the coding
CC   sequence of class V ribozyme #12 used in the method of the invention.
XX
SQ   Sequence 27 BP; 11 A; 3 C; 9 G; 4 U; 0 other;

  Query Match            100.0%;  Score 15;  DB 22;  Length 27;
  Best Local Similarity  100.0%;  Pred. No. 74;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAUAACGUGAAGAU 15
              |||||||||||||||
Db          7 AGAUAACGUGAAGAU 21


RESULT 8
AAS12301
ID   AAS12301 standard; DNA; 27 BP.
XX
AC   AAS12301;
XX
DT   21-NOV-2001  (first entry)
XX
DE   DNA encoding class V ribozyme #13.
XX
KW   Ribozyme; cytostatic; endonuclease; RNA cleavage; DNA cleavage;
KW   gene therapy; plant; fungus; bacteria; mammal; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1..6
FT                   /*tag= a
FT                   /mod_base= OTHER
FT                   /note= "OTHER = 2'-O-methyl nucleotides"
FT   modified_base   18
FT                   /*tag= b
FT                   /mod_base= a
FT                   /note= "OTHER = 2'-O-methyl nucleotide"
FT   modified_base   21..27
FT                   /*tag= c
FT                   /mod_base= OTHER
FT                   /note= "OTHER = 2'-O-methyl nucleotides"
FT   modified_base   27
FT                   /*tag= d
FT                   /mod_base= c
FT                   /note= "3',3'-inverted deoxyabasic moiety"
XX
PN   WO200159102-A2.
XX
PD   16-AUG-2001.
XX
PF   08-FEB-2001; 2001WO-US04223.
XX
PR   08-FEB-2000; 2000US-0181360.
PR   31-MAR-2000; 2000US-0193646.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
PA   (UYYA ) UNIV YALE.
XX
PI   Breaker R, Beigelman L, Emilsson G;
XX
DR   WPI; 2001-536526/59.
XX
PT   New nucleic acids with endonuclease activity, such as ribozymes and
PT   nucleozymes, for modulating gene expression in a plant, mammalian,
PT   bacterial or fungal cell -
XX
PS   Example 1; Page 71; 96pp; English.
XX
CC   The invention relates to nucleic acid molecules with endonuclease
CC   activity, which are particularly useful for cleavage of RNA or DNA.
CC   The nucleic acids are used in a pharmaceutical composition and are used
CC   to modulate expression of a gene in a plant, mammalian, bacterial or
CC   fungal cell. They are used to cleave a separate nucleic acid, preferably
CC   RNA. The nucleic acids are used to inhibit gene expression and/or cell
CC   proliferation, and can be used to treat a disease or condition. More
CC   than one nucleic acid can be independently targeted to the same or
CC   different sites in a cell. The nucleic acids may be used to study DNA.
CC   The modifications to the nucleic acids optimises their catalytic activity
CC   and can maintain or enhance their activity. They exhibit a high degree
CC   of specificity for RNA. The present sequence represents the coding
CC   sequence of class V ribozyme #13 used in the method of the invention.
XX
SQ   Sequence 27 BP; 11 A; 3 C; 9 G; 4 U; 0 other;

  Query Match            100.0%;  Score 15;  DB 22;  Length 27;
  Best Local Similarity  100.0%;  Pred. No. 74;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAUAACGUGAAGAU 15
              |||||||||||||||
Db          7 AGAUAACGUGAAGAU 21


RESULT 9
AAS12302
ID   AAS12302 standard; DNA; 27 BP.
XX
AC   AAS12302;
XX
DT   21-NOV-2001  (first entry)
XX
DE   DNA encoding class V ribozyme #14.
XX
KW   Ribozyme; cytostatic; endonuclease; RNA cleavage; DNA cleavage;
KW   gene therapy; plant; fungus; bacteria; mammal; ss.
XX
OS   Synthetic.
```

```
XX
FH   Key             Location/Qualifiers
FT   modified_base   1..6
FT                   /*tag= a
FT                   /mod_base= OTHER
FT                   /note= "OTHER = 2'-O-methyl nucleotides"
FT   modified_base   17
FT                   /*tag= b
FT                   /mod_base= a
FT                   /note= "OTHER = 2'-O-methyl nucleotide"
FT   modified_base   21..27
FT                   /*tag= c
FT                   /mod_base= OTHER
FT                   /note= "OTHER = 2'-O-methyl nucleotides"
FT   modified_base   27
FT                   /*tag= d
FT                   /mod_base= c
FT                   /note= "3',3'-inverted deoxyabasic moiety"
XX
PN   WO200159102-A2.
XX
PD   16-AUG-2001.
XX
PF   08-FEB-2001; 2001WO-US04223.
XX
PR   08-FEB-2000; 2000US-0181360.
PR   31-MAR-2000; 2000US-0193646.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
PA   (UYYA ) UNIV YALE.
XX
PI   Breaker R,  Beigelman L,  Emilsson G;
XX
DR   WPI; 2001-536526/59.
XX
PT   New nucleic acids with endonuclease activity, such as ribozymes and
PT   nucleozymes, for modulating gene expression in a plant, mammalian,
PT   bacterial or fungal cell  -
XX
PS   Example 1; Page 71; 96pp; English.
XX
CC   The invention relates to nucleic acid molecules with endonuclease
CC   activity, which are particularly useful for cleavage of RNA or DNA.
CC   The nucleic acids are used in a pharmaceutical composition and are used
CC   to modulate expression of a gene in a plant, mammalian, bacterial or
CC   fungal cell. They are used to cleave a separate nucleic acid, preferably
CC   RNA. The nucleic acids are used to inhibit gene expression and/or cell
CC   proliferation, and can be used to treat a disease or condition. More
CC   than one nucleic acid can be independently targeted to the same or
CC   different sites in a cell. The nucleic acids may be used to study DNA.
CC   The modifications to the nucleic acids optimises their catalytic activity
CC   and can maintain or enhance their activity. They exhibit a high degree
CC   of specificity for RNA. The present sequence represents the coding
CC   sequence of class V ribozyme #14 used in the method of the invention.
XX
SQ   Sequence 27 BP; 11 A; 3 C; 9 G; 4 U; 0 other;

  Query Match            100.0%;  Score 15;  DB 22;  Length 27;
  Best Local Similarity  100.0%;  Pred. No. 74;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAUAACGUGAAGAU 15
              |||||||||||||||
Db          7 AGAUAACGUGAAGAU 21


RESULT 10
AAS12303
ID   AAS12303 standard; DNA; 27 BP.
XX
AC   AAS12303;
XX
DT   21-NOV-2001  (first entry)
XX
DE   DNA encoding class V ribozyme #15.
XX
KW   Ribozyme; cytostatic; endonuclease; RNA cleavage; DNA cleavage;
KW   gene therapy; plant; fungus; bacteria; mammal; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1..6
FT                   /*tag= a
FT                   /mod_base= OTHER
FT                   /note= "OTHER = 2'-O-methyl nucleotides"
FT   modified_base   11
FT                   /*tag= b
FT                   /mod_base= a
FT                   /note= "OTHER = 2'-O-methyl nucleotide"
FT   modified_base   16
FT                   /*tag= c
FT                   /mod_base= g
FT                   /note= "OTHER = 2'-O-methyl nucleotide"
FT   modified_base   21..27
FT                   /*tag= d
FT                   /mod_base= OTHER
FT                   /note= "OTHER = 2'-O-methyl nucleotides"
FT   modified_base   27
FT                   /*tag= e
FT                   /mod_base= c
FT                   /note= "3',3'-inverted deoxyabasic moiety"
XX
PN   WO200159102-A2.
XX
PD   16-AUG-2001.
XX
PF   08-FEB-2001; 2001WO-US04223.
XX
PR   08-FEB-2000; 2000US-0181360.
PR   31-MAR-2000; 2000US-0193646.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
PA   (UYYA ) UNIV YALE.
XX
PI   Breaker R,  Beigelman L,  Emilsson G;
XX
DR   WPI; 2001-536526/59.
XX
PT   New nucleic acids with endonuclease activity, such as ribozymes and
PT   nucleozymes, for modulating gene expression in a plant, mammalian,
PT   bacterial or fungal cell  -
XX
PS   Example 1; Page 71; 96pp; English.
XX
CC   The invention relates to nucleic acid molecules with endonuclease
CC   activity, which are particularly useful for cleavage of RNA or DNA.
CC   The nucleic acids are used in a pharmaceutical composition and are used
CC   to modulate expression of a gene in a plant, mammalian, bacterial or
CC   fungal cell. They are used to cleave a separate nucleic acid, preferably
CC   RNA. The nucleic acids are used to inhibit gene expression and/or cell
CC   proliferation, and can be used to treat a disease or condition. More
CC   than one nucleic acid can be independently targeted to the same or
CC   different sites in a cell. The nucleic acids may be used to study DNA.
CC   The modifications to the nucleic acids optimises their catalytic activity
CC   and can maintain or enhance their activity. They exhibit a high degree
CC   of specificity for RNA. The present sequence represents the coding
CC   sequence of class V ribozyme #15 used in the method of the invention.
XX
SQ   Sequence 27 BP; 11 A; 3 C; 9 G; 4 U; 0 other;

  Query Match            100.0%;  Score 15;  DB 22;  Length 27;
  Best Local Similarity  100.0%;  Pred. No. 74;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAUAACGUGAAGAU 15
```

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                  ||||||||||||||||
Db          7 AGAUAACGUGAAGAU 21


RESULT 11
AAS12304
ID   AAS12304 standard; DNA; 27 BP.
XX
AC   AAS12304;
XX
DT   21-NOV-2001  (first entry)
XX
DE   DNA encoding class V ribozyme #16.
XX
KW   Ribozyme; cytostatic; endonuclease; RNA cleavage; DNA cleavage;
KW   gene therapy; plant; fungus; bacteria; mammal; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1..6
FT                   /*tag= a
FT                   /mod_base= OTHER
FT                   /note= "OTHER = 2'-O-methyl nucleotides"
FT   modified_base   21..27
FT                   /*tag= b
FT                   /mod_base= OTHER
FT                   /note= "OTHER = 2'-O-methyl nucleotides"
FT   modified_base   27
FT                   /*tag= c
FT                   /mod_base= c
FT                   /note= "3',3'-inverted deoxyabasic moiety"
XX
PN   WO200159102-A2.
XX
PD   16-AUG-2001.
XX
PF   08-FEB-2001; 2001WO-US04223.
XX
PR   08-FEB-2000; 2000US-0181360.
PR   31-MAR-2000; 2000US-0193646.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
PA   (UYYA ) UNIV YALE.
XX
PI   Breaker R,  Beigelman L,  Emilsson G;
XX
DR   WPI; 2001-536526/59.
XX
PT   New nucleic acids with endonuclease activity, such as ribozymes and
PT   nucleozymes, for modulating gene expression in a plant, mammalian,
PT   bacterial or fungal cell  -
XX
PS   Example 1; Page 71; 96pp; English.
XX
CC   The invention relates to nucleic acid molecules with endonuclease
CC   activity, which are particularly useful for cleavage of RNA or DNA.
CC   The nucleic acids are used in a pharmaceutical composition and are used
CC   to modulate expression of a gene in a plant, mammalian, bacterial or
CC   fungal cell. They are used to cleave a separate nucleic acid, preferably
CC   RNA. The nucleic acids are used to inhibit gene expression and/or cell
CC   proliferation, and can be used to treat a disease or condition. More
CC   than one nucleic acid can be independently targeted to the same or
CC   different sites in a cell. The nucleic acids may be used to study DNA.
CC   The modifications to the nucleic acids optimises their catalytic activity
CC   and can maintain or enhance their activity. They exhibit a high degree
CC   of specificity for RNA. The present sequence represents the coding
CC   sequence of class V ribozyme #16 used in the method of the invention.
XX
SQ   Sequence 27 BP; 11 A; 3 C; 9 G; 4 U; 0 other;

  Query Match           100.0%;  Score 15;  DB 22;  Length 27;
  Best Local Similarity  100.0%;  Pred. No. 74;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAUAACGUGAAGAU 15
                ||||||||||||||||
Db          7 AGAUAACGUGAAGAU 21


RESULT 12
AAS12305
ID   AAS12305 standard; DNA; 27 BP.
XX
AC   AAS12305;
XX
DT   21-NOV-2001  (first entry)
XX
DE   DNA encoding class V ribozyme #17.
XX
KW   Ribozyme; cytostatic; endonuclease; RNA cleavage; DNA cleavage;
KW   gene therapy; plant; fungus; bacteria; mammal; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1..6
FT                   /*tag= a
FT                   /mod_base= OTHER
FT                   /note= "OTHER = 2'-O-methyl nucleotides"
FT   modified_base   19
FT                   /*tag= b
FT                   /mod_base= g
FT                   /note= "OTHER = 2'-O-methyl nucleotide"
FT   modified_base   21..27
FT                   /*tag= c
FT                   /mod_base= OTHER
FT                   /note= "OTHER = 2'-O-methyl nucleotides"
FT   modified_base   27
FT                   /*tag= d
FT                   /mod_base= c
FT                   /note= "3',3'-inverted deoxyabasic moiety"
XX
PN   WO200159102-A2.
XX
PD   16-AUG-2001.
XX
PF   08-FEB-2001; 2001WO-US04223.
XX
PR   08-FEB-2000; 2000US-0181360.
PR   31-MAR-2000; 2000US-0193646.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
PA   (UYYA ) UNIV YALE.
XX
PI   Breaker R,  Beigelman L,  Emilsson G;
XX
DR   WPI; 2001-536526/59.
XX
PT   New nucleic acids with endonuclease activity, such as ribozymes and
PT   nucleozymes, for modulating gene expression in a plant, mammalian,
PT   bacterial or fungal cell  -
XX
PS   Example 1; Page 71; 96pp; English.
XX
CC   The invention relates to nucleic acid molecules with endonuclease
CC   activity, which are particularly useful for cleavage of RNA or DNA.
CC   The nucleic acids are used in a pharmaceutical composition and are used
CC   to modulate expression of a gene in a plant, mammalian, bacterial or
CC   fungal cell. They are used to cleave a separate nucleic acid, preferably
CC   RNA. The nucleic acids are used to inhibit gene expression and/or cell
CC   proliferation, and can be used to treat a disease or condition. More
CC   than one nucleic acid can be independently targeted to the same or
CC   different sites in a cell. The nucleic acids may be used to study DNA.
CC   The modifications to the nucleic acids optimises their catalytic activity
CC   and can maintain or enhance their activity. They exhibit a high degree
```

```
CC   of specificity for RNA. The present sequence represents the coding
CC   sequence of class V ribozyme #17 used in the method of the invention.
XX
SQ   Sequence 27 BP; 11 A; 3 C; 9 G; 4 U; 0 other;

  Query Match             100.0%;  Score 15;  DB 22;  Length 27;
  Best Local Similarity   100.0%;  Pred. No. 74;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAUAACGUGAAGAU 15
              |||||||||||||||
Db          7 AGAUAACGUGAAGAU 21


RESULT 13
AAS12306
ID   AAS12306 standard; DNA; 27 BP.
XX
AC   AAS12306;
XX
DT   21-NOV-2001  (first entry)
XX
DE   DNA encoding class V ribozyme #18.
XX
KW   Ribozyme; cytostatic; endonuclease; RNA cleavage; DNA cleavage;
KW   gene therapy; plant; fungus; bacteria; mammal; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1..6
FT                   /*tag= a
FT                   /mod_base= OTHER
FT                   /note= "OTHER = 2'-O-methyl nucleotides"
FT   modified_base   14
FT                   /*tag= b
FT                   /mod_base= g
FT                   /note= "OTHER = 2'-O-methyl nucleotide"
FT   modified_base   21..27
FT                   /*tag= c
FT                   /mod_base= OTHER
FT                   /note= "OTHER = 2'-O-methyl nucleotides"
FT   modified_base   27
FT                   /*tag= d
FT                   /mod_base= c
FT                   /note= "3',3'-inverted deoxyabasic moiety"
XX
PN   WO200159102-A2.
XX
PD   16-AUG-2001.
XX
PF   08-FEB-2001; 2001WO-US04223.
XX
PR   08-FEB-2000; 2000US-0181360.
PR   31-MAR-2000; 2000US-0193646.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
PA   (UYYA ) UNIV YALE.
XX
PI   Breaker R,  Beigelman L,  Emilsson G;
XX
DR   WPI; 2001-536526/59.
XX
PT   New nucleic acids with endonuclease activity, such as ribozymes and
PT   nucleozymes, for modulating gene expression in a plant, mammalian,
PT   bacterial or fungal cell  -
XX
PS   Example 1; Page 71; 96pp; English.
XX
CC   The invention relates to nucleic acid molecules with endonuclease
CC   activity, which are particularly useful for cleavage of RNA or DNA.
CC   The nucleic acids are used in a pharmaceutical composition and are used
CC   to modulate expression of a gene in a plant, mammalian, bacterial or
CC   fungal cell. They are used to cleave a separate nucleic acid, preferably
CC   RNA. The nucleic acids are used to inhibit gene expression and/or cell
CC   proliferation, and can be used to treat a disease or condition. More
CC   than one nucleic acid can be independently targeted to the same or
CC   different sites in a cell. The nucleic acids may be used to study DNA.
CC   The modifications to the nucleic acids optimises their catalytic activity
CC   and can maintain or enhance their activity. They exhibit a high degree
CC   of specificity for RNA. The present sequence represents the coding
CC   sequence of class V ribozyme #18 used in the method of the invention.
XX
SQ   Sequence 27 BP; 11 A; 3 C; 9 G; 4 U; 0 other;

  Query Match             100.0%;  Score 15;  DB 22;  Length 27;
  Best Local Similarity   100.0%;  Pred. No. 74;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAUAACGUGAAGAU 15
              |||||||||||||||
Db          7 AGAUAACGUGAAGAU 21


RESULT 14
AAS12307
ID   AAS12307 standard; DNA; 27 BP.
XX
AC   AAS12307;
XX
DT   21-NOV-2001  (first entry)
XX
DE   DNA encoding class V ribozyme #19.
XX
KW   Ribozyme; cytostatic; endonuclease; RNA cleavage; DNA cleavage;
KW   gene therapy; plant; fungus; bacteria; mammal; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1..6
FT                   /*tag= a
FT                   /mod_base= OTHER
FT                   /note= "OTHER = 2'-O-methyl nucleotides"
FT   modified_base   13
FT                   /*tag= b
FT                   /mod_base= c
FT                   /note= "OTHER = 2'-O-methyl nucleotide"
FT   modified_base   21..27
FT                   /*tag= c
FT                   /mod_base= OTHER
FT                   /note= "OTHER = 2'-O-methyl nucleotides"
FT   modified_base   27
FT                   /*tag= d
FT                   /mod_base= c
FT                   /note= "3',3'-inverted deoxyabasic moiety"
XX
PN   WO200159102-A2.
XX
PD   16-AUG-2001.
XX
PF   08-FEB-2001; 2001WO-US04223.
XX
PR   08-FEB-2000; 2000US-0181360.
PR   31-MAR-2000; 2000US-0193646.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
PA   (UYYA ) UNIV YALE.
XX
PI   Breaker R,  Beigelman L,  Emilsson G;
XX
DR   WPI; 2001-536526/59.
XX
PT   New nucleic acids with endonuclease activity, such as ribozymes and
PT   nucleozymes, for modulating gene expression in a plant, mammalian,
PT   bacterial or fungal cell  -
```

```
XX
PS   Example 1; Page 71; 96pp; English.
XX
CC   The invention relates to nucleic acid molecules with endonuclease
CC   activity, which are particularly useful for cleavage of RNA or DNA.
CC   The nucleic acids are used in a pharmaceutical composition and are used
CC   to modulate expression of a gene in a plant, mammalian, bacterial or
CC   fungal cell. They are used to cleave a separate nucleic acid, preferably
CC   RNA. The nucleic acids are used to inhibit gene expression and/or cell
CC   proliferation, and can be used to treat a disease or condition. More
CC   than one nucleic acid can be independently targeted to the same or
CC   different sites in a cell. The nucleic acids may be used to study DNA.
CC   The modifications to the nucleic acids optimises their catalytic activity
CC   and can maintain or enhance their activity. They exhibit a high degree
CC   of specificity for RNA. The present sequence represents the coding
CC   sequence of class V ribozyme #19 used in the method of the invention.
XX
SQ   Sequence 27 BP; 11 A; 3 C; 9 G; 4 U; 0 other;

  Query Match             100.0%;  Score 15;  DB 22;  Length 27;
  Best Local Similarity   100.0%;  Pred. No. 74;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAUAACGUGAAGAU 15
              |||||||||||||||
Db          7 AGAUAACGUGAAGAU 21


RESULT 15
AAS12308
ID   AAS12308 standard; DNA; 27 BP.
XX
AC   AAS12308;
XX
DT   21-NOV-2001  (first entry)
XX
DE   DNA encoding class V ribozyme #20.
XX
KW   Ribozyme; cytostatic; endonuclease; RNA cleavage; DNA cleavage;
KW   gene therapy; plant; fungus; bacteria; mammal; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1..6
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "OTHER = 2'-O-methyl nucleotides"
FT   modified_base   21..27
FT                   /*tag=  b
FT                   /mod_base= OTHER
FT                   /note= "OTHER = 2'-O-methyl nucleotides"
FT   modified_base   27
FT                   /*tag=  c
FT                   /mod_base= c
FT                   /note= "3',3'-inverted deoxyabasic moiety"
XX
PN   WO200159102-A2.
XX
PD   16-AUG-2001.
XX
PF   08-FEB-2001; 2001WO-US04223.
XX
PR   08-FEB-2000; 2000US-0181360.
PR   31-MAR-2000; 2000US-0193646.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
PA   (UYYA ) UNIV YALE.
XX
PI   Breaker R,  Beigelman L,  Emilsson G;
XX
DR   WPI; 2001-536526/59.
XX
PT   New nucleic acids with endonuclease activity, such as ribozymes and
PT   nucleozymes, for modulating gene expression in a plant, mammalian,
PT   bacterial or fungal cell  -
XX
PS   Example 1; Page 71; 96pp; English.
XX
CC   The invention relates to nucleic acid molecules with endonuclease
CC   activity, which are particularly useful for cleavage of RNA or DNA.
CC   The nucleic acids are used in a pharmaceutical composition and are used
CC   to modulate expression of a gene in a plant, mammalian, bacterial or
CC   fungal cell. They are used to cleave a separate nucleic acid, preferably
CC   RNA. The nucleic acids are used to inhibit gene expression and/or cell
CC   proliferation, and can be used to treat a disease or condition. More
CC   than one nucleic acid can be independently targeted to the same or
CC   different sites in a cell. The nucleic acids may be used to study DNA.
CC   The modifications to the nucleic acids optimises their catalytic activity
CC   and can maintain or enhance their activity. They exhibit a high degree
CC   of specificity for RNA. The present sequence represents the coding
CC   sequence of class V ribozyme #20 used in the method of the invention.
XX
SQ   Sequence 27 BP; 11 A; 3 C; 9 G; 4 U; 0 other;

  Query Match             100.0%;  Score 15;  DB 22;  Length 27;
  Best Local Similarity   100.0%;  Pred. No. 74;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAUAACGUGAAGAU 15
              |||||||||||||||
Db          7 AGAUAACGUGAAGAU 21


Search completed: July  6, 2003, 14:32:52
Job time : 160.909 secs
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: July 6, 2003, 14:26:51 ; Search time 1007.73 Seconds
(without alignments)
241.069 Million cell updates/sec

Title: US-09-780-929-97
Perfect score: 15
Sequence: 1 agauaacgugaagau 15

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 146654

Minimum DB seq length: 0
Maximum DB seq length: 60

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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1: em_estba:*
2: em_esthum:*
3: em_estin:*
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5: em_estov:*
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7: em_estro:*
8: em_htc:*
9: gb_est1:*
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12: gb_est3:*
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20: em_gss_pln:*
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22: em_gss_fun:*
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25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
c	1	11.8	78.7	29	17	AZ994980	AZ994980 2M0280G07
	2	11.8	78.7	59	14	BQ625912	BQ625912 ph86f02.y
c	3	10.8	72.0	22	17	TA248D01P	AL483187 T. brucei
	4	10.8	72.0	28	17	AZ345853	AZ345853 1M0080F14
	5	10.8	72.0	37	9	AA947987	AA947987 oq58e02.s
	6	10.8	72.0	37	17	AL760544	AL760544 Arabidops
c	7	10.8	72.0	40	9	AI039249	AI039249 ox33a08.s
	8	10.8	72.0	46	17	AZ482955	AZ482955 1M0308M13
	9	10.8	72.0	48	17	AZ656367	AZ656367 1M0531D23
	10	10.8	72.0	48	17	AZ772291	AZ772291 1M0583L06
c	11	10.8	72.0	50	9	AU103231	AU103231 AU103231
	12	10.8	72.0	51	10	AV833384	AV833384 AV833384
	13	10.8	72.0	52	9	AA823664	AA823664 vr69d09.s
c	14	10.8	72.0	52	12	BF631905	BF631905 NF016H07D
	15	10.8	72.0	53	9	AU257573	AU257573 AU257573
c	16	10.8	72.0	54	13	BM069548	BM069548 ie89d12.x
c	17	10.8	72.0	54	17	AF149434	AF149434 AF149434
	18	10.8	72.0	58	9	AA780323	AA780323 af52b09.s
	19	10.8	72.0	59	13	BJ053305	BJ053305 BJ053305
	20	10.4	69.3	42	13	BJ044345	BJ044345 BJ044345
	21	10.4	69.3	44	14	D18694	D18694 MUSGS01756
	22	10.4	69.3	48	14	D18688	D18688 MUSGS01750
	23	10.4	69.3	51	10	AW100987	AW100987 sd64b07.y
	24	10.4	69.3	53	17	AL764237	AL764237 Arabidops
c	25	10.4	69.3	55	10	AW424064	AW424064 sh60c04.y
	26	10.4	69.3	56	12	BG731546	BG731546 dac26g09.
c	27	10.4	69.3	56	17	AZ784261	AZ784261 2M0026H22
	28	10.4	69.3	57	9	AU256712	AU256712 AU256712
	29	10.4	69.3	58	9	AA265174	AA265174 mz49h04.r
c	30	10.4	69.3	60	13	BI493320	BI493320 df99g12.y
c	31	10.4	69.3	60	17	AL752372	AL752372 Arabidops
	32	10.2	68.0	19	17	AZ759898	AZ759898 1M0553A08
c	33	10.2	68.0	24	17	TA200H11P	AL475521 T. brucei
c	34	10.2	68.0	33	17	AL760055	AL760055 Arabidops
	35	10.2	68.0	37	17	AZ760010	AZ760010 1M0553D21
c	36	10.2	68.0	40	9	AI609205	AI609205 tw83a05.x
c	37	10.2	68.0	40	9	AI638565	AI638565 ts50b02.x
	38	10.2	68.0	40	14	N54453	N54453 yv40a04.s1
	39	10.2	68.0	42	17	AZ388234	AZ388234 1M0148E12
c	40	10.2	68.0	42	17	AZ449920	AZ449920 1M0248I20
c	41	10.2	68.0	44	12	BE738334	BE738334 601572718
	42	10.2	68.0	45	17	BH638406	BH638406 1008022D0
	43	10.2	68.0	46	9	AI077563	AI077563 oz33g04.x
c	44	10.2	68.0	46	17	AZ321153	AZ321153 1M0041M11
c	45	10.2	68.0	48	17	BH863621	BH863621 SALK_0942

ALIGNMENTS

RESULT 1
AZ994980/c
LOCUS AZ994980 29 bp DNA linear GSS 27-APR-2001
DEFINITION 2M0280G07R Mouse 10kb plasmid UUGC2M library Mus musculus genomic clone UUGC2M0280G07 R, DNA sequence.
ACCESSION AZ994980
VERSION AZ994980.1 GI:13866207
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 29)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00

Plate: 0280 row: G column: 07
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 29.

FEATURES Location/Qualifiers
source 1. .29
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0280G07"
/clone_lib="Mouse 10kb plasmid UUGC2M library"
/sex="Female"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 5 a 5 c 5 g 14 t
ORIGIN

Query Match 78.7%; Score 11.8; DB 17; Length 29;
Best Local Similarity 66.7%; Pred. No. 1.2e+04;
Matches 10; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AGAUAACGUGAAGAU 15
||| :| |:|||||:
Db 23 AGATAGAGTGAAGAT 9

RESULT 2
BQ625912
LOCUS BQ625912 59 bp mRNA linear EST 01-JUL-2002
DEFINITION ph86f02.y1 Ostertagia ostertagi L3 SL1 TOPO v2 Ostertagia ostertagi cDNA 5', mRNA sequence.
ACCESSION BQ625912
VERSION BQ625912.1 GI:21653090
KEYWORDS EST.
SOURCE Ostertagia ostertagi.
ORGANISM Ostertagia ostertagi
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Strongylida; Trichostrongyloidea; Haemonchidae; Ostertagiinae; Ostertagia.
REFERENCE 1 (bases 1 to 59)
AUTHORS McCarter,J., Clifton,S., Chiapelli,B., Pape,D., Martin,J., Wylie,T., Dante,M., Marra,M., Hillier,L., Kucaba,T., Theising,B., Bowers,Y., Gibbons,M., Ritter,E., Bennett,J., Franklin,C., Tsagareishvili,R., Ronko,I., Kennedy,S., Maguire,L., Beck,C., Underwood,K., Steptoe,M., Allen,M., Person,B., Swaller,T., Harvey,N., Schurk,R., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.
TITLE The Washington Univ. Nematode EST Project, 1999
JOURNAL Unpublished (1999)
COMMENT Contact: McCarter JP
The Washington Univ. Nematode EST Project, 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
The library was constructed by Claire Murphy and Dr. James McCarter at Washington University, St. Louis. Nematodes were provided by Dr. Louis Gasbarree of the USDA, Beltsville, MD (lgasbarr@anri.barc.usda.gov).
Putative full length read
The vector to vector length is 60
Seq primer: SL1 primer.

FEATURES Location/Qualifiers
source 1. .59
/organism="Ostertagia ostertagi"
/db_xref="taxon:6317"
/clone_lib="Ostertagia ostertagi L3 SL1 TOPO v2"
/dev_stage="third stage exsheathed larvae"
/lab_host="DH10B"
/note="Vector: pCRII-TOPO (Invitrogen); Site_1: EcoRI; Site_2: EcoRI; The library was constructed by Claire Murphy and Dr. James McCarter at Washington University, St. Louis. Oligo(dT)-SL1 PCR based library. Ostertagia ostertagi L3 cDNA PCR products of size >400 nucleotides containing SL1 on the 5' end and oligo(dT) on the 3' end were non-directionally cloned into pCRII-TOPO(Invitrogen) following the Topo TA cloning protocol. Nematodes were provided by Dr. Louis Gasbarree of the USDA, Beltsville, MD (lgasbarr@anri.barc.usda.gov). Third stage exsheathed larvae were collected from 14 day fecal-sphagnum moss cultures of Ostertagia eggs. The larvae were recovered by overnight passage on a Baermann apparatus, and then cleaned by passage through a 20 micron nylon mesh. The larvae were then subjected to a treatment with 1.25% chlorox to induce excystation. The larvae were washed with 5 changes of PBS and then pelleted and snap frozen in liquid nitrogen."

BASE COUNT 22 a 16 c 12 g 9 t
ORIGIN

Query Match 78.7%; Score 11.8; DB 14; Length 59;
Best Local Similarity 73.3%; Pred. No. 1.7e+04;
Matches 11; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AGAUAACGUGAAGAU 15
||| || |:|||||:
Db 7 AGAAAAGGTGAAGAT 21

RESULT 3
TA248D01P/c
LOCUS TA248D01P 22 bp DNA linear GSS 13-DEC-2000
DEFINITION T. brucei sheared genomic DNA clone 248d01, forward sequence, genomic survey sequence.
ACCESSION AL483187
VERSION AL483187.1 GI:11848863
KEYWORDS GSS.
SOURCE Trypanosoma brucei.
ORGANISM Trypanosoma brucei
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
REFERENCE 1 (bases 1 to 22)
AUTHORS Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R., Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L., Melville,S.E., Rajandream,M.A. and Barrell,B.G.
TITLE Direct Submission
JOURNAL Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and nh1@sanger.ac.uk
COMMENT Constructed at the Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a cloned population of Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared to give a tight size distribution (
4 kb). The v + i method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.

Barrell, Oxford University Press, 1999).
Email: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available at http://www.sanger.ac.uk/Projects/T_brucei/.

FEATURES Location/Qualifiers
source 1. .22
/organism="Trypanosoma brucei"
/strain="TREU927"
/db_xref="taxon:5691"
/clone="248d01"

BASE COUNT 5 a 6 c 2 g 9 t
ORIGIN

Query Match 72.0%; Score 10.8; DB 17; Length 22;
Best Local Similarity 64.3%; Pred. No. 3.8e+04;
Matches 9; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 2 GAUAACGUGAAGAU 15
||:||| :||| |:
Db 19 GATAACATGAAAAT 6

RESULT 4
AZ345853
LOCUS AZ345853 28 bp DNA linear GSS 29-SEP-2000
DEFINITION 1M0080F14R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0080F14 R, DNA sequence.
ACCESSION AZ345853
VERSION AZ345853.1 GI:10425090
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 28)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0080 row: F column: 14
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 28.

FEATURES Location/Qualifiers
source 1. .28
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0080F14"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 16 a 3 c 4 g 5 t
ORIGIN

Query Match 72.0%; Score 10.8; DB 17; Length 28;
Best Local Similarity 71.4%; Pred. No. 4.3e+04;
Matches 10; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AGAUAACGUGAAGA 14
| |:||||:||| |
Db 9 AAATAACGTGAAAA 22

RESULT 5
AA947987
LOCUS AA947987 37 bp mRNA linear EST 04-MAY-1998
DEFINITION oq58e02.s1 NCI_CGAP_Kid6 Homo sapiens cDNA clone IMAGE:1590554 3' similar to TR:Q33559 Q33559 NH2 TERMINUS UNCERTAIN ;, mRNA sequence.
ACCESSION AA947987
VERSION AA947987.1 GI:3109240
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 37)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: L. Jeffrey Medeiros, M.D., Michael R. Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: Stratagene, Inc.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality
Seq primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 1.

FEATURES Location/Qualifiers
source 1. .37
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1590554"
/clone_lib="NCI_CGAP_Kid6"
/sex="mixed"
/tissue_type="kidney tumor"
/lab_host="SOLR (kanamycin resistant)"
/note="Organ: kidney; Vector: Bluescript SK-; Site_1: EcoRI; Site_2: XhoI; Cloned unidirectionally. Primer: Oligo dT. Pooled kidney tumors. 5' adaptor sequence: 5' GAATTCGGCACGAG 3' 3' adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTTT 3' Average insert size: 1.0 kb."

BASE COUNT 26 a 2 c 6 g 3 t
ORIGIN

Query Match 72.0%; Score 10.8; DB 9; Length 37;
Best Local Similarity 78.6%; Pred. No. 4.9e+04;

```
  Matches   11;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 AGAUAACGUGAAGA 14
              |||:|| | |||||
Db         17 AGATAATGAGAAGA 30


RESULT 6
AL760544
LOCUS       AL760544                37 bp    DNA     linear   GSS 19-JUN-2002
DEFINITION  Arabidopsis thaliana T-DNA flanking sequence GK-199B11-014765,
            genomic survey sequence.
ACCESSION   AL760544
VERSION     AL760544.1  GI:21499415
KEYWORDS    GSS.
SOURCE      thale cress.
  ORGANISM  Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1
  AUTHORS   Strizhov,N., Li,Y., Rosso,M., Viehoever,P., Dekker,K., Saedler,H.
            and Weisshaar,B.
  TITLE     A pipeline for automated high-throughput generation of FSTs
            (flanking sequence tags) from Arabidopsis thaliana T-DNA
            transformed lines
  JOURNAL   Unpublished
REFERENCE   2
  AUTHORS   Rosso,M., Strizhov,N., Li,Y., Reiss,B., Dekker,K. and Weisshaar,B.
  TITLE     A new Arabidopsis thaliana T-DNA mutagenised population (GABI-Kat)
            for flanking sequence tag based reverse genetics
  JOURNAL   Unpublished
REFERENCE   3  (bases 1 to 37)
  AUTHORS   Li,Y., Strizhov,N., Rosso,M. and Weisshaar,B.
  TITLE     Direct Submission
  JOURNAL   Submitted (17-JUN-2002) Weisshaar B., Max-Planck-Institut fuer
            Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany
COMMENT     This sequence is recovered from the left border of the T-DNA. It
            indicates an insertion close to or within gene At1g77800. The
            sequences are generated at the MPI for Plant Breeding Research in
            the context of the GABI-Kat project. GABI-Kat is part of the German
            Plant Genomics program designated 'GABI'. Information on line
            availability can be found at:
            http://www.mpiz-koeln.mpg.de/GABI-Kat/.
FEATURES             Location/Qualifiers
     source          1. .37
                     /organism="Arabidopsis thaliana"
                     /strain="Columbia 0"
                     /db_xref="taxon:3702"
                     /clone="GK-199B11-014765"
                     /clone_lib="Arabidopsis thaliana T-DNA insertion lines"
                     /note="PCR was performed on DNA from Arabidopsis thaliana
                     plants (T1) which were transformed with the T-DNA from
                     vector pAC161. The lines contain one or more T-DNA
                     insertions. The DNA fragment(s) resulting from the PCR
                     were directly sequenced to determine the genomic sequence
                     flanking the insertion. Sequences displaying significant
                     similarity to the A. thalaina nuclear genome sequence were
                     processed for submission. T-DNA derived sequences were
                     removed"
BASE COUNT      19 a      4 c      6 g      8 t
ORIGIN

  Query Match           72.0%;  Score 10.8;  DB 17;  Length 37;
  Best Local Similarity 78.6%;  Pred. No. 4.9e+04;
  Matches   11;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 AGAUAACGUGAAGA 14
              ||| ||| :|||||
Db         21 AGAAAACATGAAGA 34


RESULT 7
AI039249/c
LOCUS       AI039249                40 bp    mRNA    linear   EST 30-JUN-1998
DEFINITION  ox33a08.s1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone
            IMAGE:1658102 3' similar to TR:O00554 O00554 P21-ARC. [1] ;, mRNA
            sequence.
ACCESSION   AI039249
VERSION     AI039249.1  GI:3278443
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 40)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Trace considered overall poor quality
            Seq primer: -40m13 fwd. ET from Amersham
            High quality sequence stop: 1.
FEATURES             Location/Qualifiers
     source          1. .40
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:1658102"
                     /clone_lib="Soares_total_fetus_Nb2HF8_9w"
                     /dev_stage="8-9 weeks"
                     /lab_host="DH10B"
                     /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                     polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
                     was prepared from mRNA obtained from pooled 8-9 week
                     (total) fetus material with a Not I - oligo(dT) primer [5'
                     TGTTACCAATCTGAAGTGGGAGCGGCCGCTTAATTTTTTTTTTTTTTTT 3'].
                     Double-stranded cDNA was ligated to Eco RI adaptors
                     (Pharmacia), digested with Not I and cloned into the Not I
                     and Eco RI sites of the modified pT7T3 vector. Library
                     went through one round of normalization, and was
                     constructed  by Bento Soares and M. Fatima Bonaldo. "
BASE COUNT       3 a      11 c      10 g      16 t
ORIGIN

  Query Match           72.0%;  Score 10.8;  DB 9;  Length 40;
  Best Local Similarity 71.4%;  Pred. No. 5.1e+04;
  Matches   10;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 AGAUAACGUGAAGA 14
              |||: |||:|| ||
Db         17 AGATGACGTGATGA 4


RESULT 8
AZ482955
LOCUS       AZ482955                46 bp    DNA     linear   GSS 05-OCT-2000
DEFINITION  1M0308M13F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0308M13 F, DNA sequence.
ACCESSION   AZ482955
VERSION     AZ482955.1  GI:10646499
KEYWORDS    GSS.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 46)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
            ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
            and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
```

```
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0308  row: M  column: 13
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 46.
FEATURES             Location/Qualifiers
     source          1. .46
                     /organism="Mus musculus"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0308M13"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."
BASE COUNT       26 a      6 c      8 g      6 t
ORIGIN

  Query Match             72.0%;  Score 10.8;  DB 17;  Length 46;
  Best Local Similarity   78.6%;  Pred. No. 5.4e+04;
  Matches   11;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 AGAUAACGUGAAGA 14
              ||| |||| :||| |
Db         19 AGAAAACGTGAAAA 32


RESULT 9
AZ656367
LOCUS       AZ656367                 48 bp    DNA     linear   GSS 14-DEC-2000
DEFINITION  1M0531D23R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0531D23 R, DNA sequence.
ACCESSION   AZ656367
VERSION     AZ656367.1  GI:11793513
KEYWORDS    GSS.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 48)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
            ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
            and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0531  row: D  column: 23
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 48.
FEATURES             Location/Qualifiers
     source          1. .48
                     /organism="Mus musculus"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0531D23"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."
BASE COUNT       26 a      8 c      6 g      8 t
ORIGIN

  Query Match             72.0%;  Score 10.8;  DB 17;  Length 48;
  Best Local Similarity   71.4%;  Pred. No. 5.6e+04;
  Matches   10;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 AGAUAACGUGAAGA 14
              | |:||||:||| |
Db         20 AAATAACGTGAAAA 33


RESULT 10
AZ772291
LOCUS       AZ772291                 48 bp    DNA     linear   GSS 16-FEB-2001
DEFINITION  1M0583L06F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0583L06 F, DNA sequence.
ACCESSION   AZ772291
VERSION     AZ772291.1  GI:12895445
KEYWORDS    GSS.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 48)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
            ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
            and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
```

```
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0583  row: L  column: 06
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 48.
FEATURES             Location/Qualifiers
     source          1. .48
                     /organism="Mus musculus"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0583L06"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance.".
BASE COUNT       23 a      8 c      7 g     10 t
ORIGIN

  Query Match             72.0%;  Score 10.8;  DB 17;  Length 48;
  Best Local Similarity   71.4%;  Pred. No. 5.6e+04;
  Matches   10;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 AGAUAACGUGAAGA 14
              | |:||||:||| |
Db         33 AAATAACGTGAAAA 46


RESULT 11
AU103231/c
LOCUS       AU103231                 50 bp    mRNA    linear   EST 30-AUG-2001
DEFINITION  AU103231 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
            KAT07952, mRNA sequence.
ACCESSION   AU103231
VERSION     AU103231.1  GI:13552752
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 50)
  AUTHORS   Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J., Hata
            ,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K., Sakaki
            ,Y., Nakamura,Y., Suyama,A. and Sugano,S.
  TITLE     Diverse transcriptional initiation revealed by fine, large-scale
            mapping of mRNA start sites
  JOURNAL   EMBO Rep. 2 (5), 388-393 (2001)
  MEDLINE   21270072
COMMENT     Contact: Yutaka Suzuki
            Department of Virology
            Institute of Medical Science, University of Tokyo
            4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
            Email: ysuzuki@ims.u-tokyo.ac.jp
            Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano
            ,S. Construction and characterization of a full length-enriched and
            a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).
FEATURES             Location/Qualifiers
     source          1. .50
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="KAT07952"
                     /clone_lib="Sugano Homo sapiens cDNA library"
                     /note="Differential display comparison of untreated and
                     dimethylfumarate treated U937 cells"
BASE COUNT       17 a     12 c      9 g     12 t
ORIGIN

  Query Match             72.0%;  Score 10.8;  DB 9;  Length 50;
  Best Local Similarity   71.4%;  Pred. No. 5.7e+04;
  Matches   10;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 GAUAACGUGAAGAU 15
              || || |:|||||:
Db         46 GAGAATGTGAAGAT 33


RESULT 12
AV833384
LOCUS       AV833384                 51 bp    mRNA    linear   EST 22-JUN-2001
DEFINITION  AV833384 K. Sato unpublished cDNA library: Hordeum vulgare subsp.
            vulgare shoots germination Hordeum vulgare subsp. vulgare cDNA
            clone bags7123, mRNA sequence.
ACCESSION   AV833384
VERSION     AV833384.1  GI:14525473
KEYWORDS    EST.
SOURCE      Hordeum vulgare subsp. vulgare.
  ORGANISM  Hordeum vulgare subsp. vulgare
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
            ; Triticeae; Hordeum.
REFERENCE   1  (bases 1 to 51)
  AUTHORS   Sato,K.
  TITLE     Barley EST sequencing project in NIG and Okayama Univ
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Kazuhiro Sato
            Research Institute for Bioresources
            Okayama University, Barley Germplasm Center
            Chuo 2-20-1, Kurashiki, Okayama 710-0046, Japan
            Email: kazsato@rib.okayama-u.ac.jp,
            URL:http://www.rib.okayama-u.ac.jp/barley/
            Sato,K., Saisho,D., Takeda,K., Shini,T. and Kohara,Y. Direct
            submission;
            database:http://www.shigen.nig.ac.jp/barley/Barley.html.
FEATURES             Location/Qualifiers
     source          1. .51
                     /organism="Hordeum vulgare subsp. vulgare"
                     /cultivar="Haruna Nijo"
                     /db_xref="taxon:112509"
                     /clone="bags7123"
                     /clone_lib="K. Sato unpublished cDNA library: Hordeum
                     vulgare subsp. vulgare shoots germination"
                     /tissue_type="shoots"
                     /dev_stage="germination"
BASE COUNT       13 a     14 c     18 g      6 t
ORIGIN

  Query Match             72.0%;  Score 10.8;  DB 10;  Length 51;
  Best Local Similarity   78.6%;  Pred. No. 5.7e+04;
  Matches   11;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;
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Qy          1 AGAUAACGUGAAGA 14
              ||| |||| :| |||
Db         36 AGAGAACGTGGAGA 49


RESULT 13
AA823664
LOCUS       AA823664                 52 bp    mRNA    linear   EST 17-FEB-1998
DEFINITION  vr69d09.s1 Knowles Solter mouse 2 cell Mus musculus cDNA clone
            IMAGE:1125905 5' similar to gb:J03161 SERUM RESPONSE FACTOR (HUMAN
            );, mRNA sequence.
ACCESSION   AA823664
VERSION     AA823664.1  GI:2893532
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 52)
  AUTHORS   Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
            Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
            Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
            Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
            Waterston,R.
  TITLE     The WashU-HHMI Mouse EST Project
  JOURNAL   Unpublished (1996)
COMMENT     Contact: Marra M/Mouse EST Project
            WashU-HHMI Mouse EST Project
            Washington University School of MedicineP
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: mouseest@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            MGI:615241.
FEATURES             Location/Qualifiers
     source          1. .52
                     /organism="Mus musculus"
                     /strain="C57BL/6J x DBA/2J F1"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:1125905"
                     /clone_lib="Knowles Solter mouse 2 cell"
                     /tissue_type="embryo"
                     /dev_stage="2-cell"
                     /lab_host="DH10B"
                     /note="Organ: embryo; Vector: pBluescribe (modified);
                     Site_1: MluI; Site_2: SalI; Cloned unidirectionally from
                     mRNA prepared from 13,500 2-cell stage  embryos.  Primer:
                     SalI(dT): 5'-CGGTCGACCGTCGACCGTTTTTTTTTTTTTT-3'.   cDNAs
                     were cloned into the MluI/SalI sites of a modified
                     pBluescribe  vector using commercial linkers (NEB).
                     Average insert size:  1.2 kb."
BASE COUNT       26 a      3 c      6 g     17 t
ORIGIN

  Query Match             72.0%;  Score 10.8;  DB 9;  Length 52;
  Best Local Similarity   71.4%;  Pred. No. 5.8e+04;
  Matches   10;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 AGAUAACGUGAAGA 14
              |||: |||:||| |
Db          3 AGATGACGTGAAAA 16


RESULT 14
BF631905/c
LOCUS       BF631905                 52 bp    mRNA    linear   EST 19-DEC-2000
DEFINITION  NF016H07DT1F1061 Drought Medicago truncatula cDNA clone NF016H07DT
            5', mRNA sequence.
ACCESSION   BF631905
VERSION     BF631905.1  GI:11896063
KEYWORDS    EST.
SOURCE      barrel medic.
  ORGANISM  Medicago truncatula
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
            Medicago.
REFERENCE   1  (bases 1 to 52)
  AUTHORS   Torrez-Jerez,I., Scott,A.D., Harris,A.R., Gonzales,R.A., Bell,C.J.,
            Flores,H.R., Inman,J.T., Weller,J.W. and May,G.D.
  TITLE     Expressed Sequence Tags from the Samuel Roberts Noble Foundation
            Medicago truncatula drought library
  JOURNAL   Unpublished (2000)
COMMENT     Contact: May GD
            Plant Biology Division
            The Samuel Roberts Noble Foundation
            2510 Sam Noble Parkway, Ardmore, OK 73402, USA
            Tel: 580 221 7391
            Fax: 580 221 7380
            Email: gdmay@noble.org
            Insert Length: 52   Std Error: 0.00
            Plate: 016  row: H  column: 07
            Seq primer: TCACACAGGAAACAGCTATGAC.
FEATURES             Location/Qualifiers
     source          1. .52
                     /organism="Medicago truncatula"
                     /db_xref="taxon:3880"
                     /clone="NF016H07DT"
                     /clone_lib="Drought"
                     /tissue_type="Plantlets"
                     /dev_stage="Pooled timepoints"
                     /note="Vector: Lambda Zap; Contains a mixture of entire
                     plantlets harvested in a series of days-post-watering
                     timepoints. "
BASE COUNT       11 a      15 c      5 g     21 t
ORIGIN

  Query Match             72.0%;  Score 10.8;  DB 12;  Length 52;
  Best Local Similarity   71.4%;  Pred. No. 5.8e+04;
  Matches   10;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 GAUAACGUGAAGAU 15
              ||:|| | |||||:
Db         48 GATAAAGAGAAGAT 35


RESULT 15
AU257573
LOCUS       AU257573                 53 bp    mRNA    linear   EST 25-APR-2002
DEFINITION  AU257573 3'-directed mouse cDNA library Mus musculus cDNA clone
            BED0010931 3', mRNA sequence.
ACCESSION   AU257573
VERSION     AU257573.1  GI:20322326
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 53)
  AUTHORS   Kato,K. and Matoba,R.
  TITLE     Generation of expressed sequence tags from mouse brain
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Kikuya Kato
            Graduate School of Biological Sciences
            Nara Institute of Science and Technology
            8916-5 Takayama, Ikoma, Nara 630-0101, Japan
            Tel: 81-743-72-5581
            Fax: 81-743-72-5589
            Email: kkato@bs.aist-nara.ac.jp,
            URL:http://love2.aist-nara.ac.jp/BED/index.html.
FEATURES             Location/Qualifiers
     source          1. .53
                     /organism="Mus musculus"
                     /db_xref="taxon:10090"
```

/clone="BED0010931"
/clone_lib="3'-directed mouse cDNA library"
/tissue_type="brain"
/note="Vector: pGEM-T-easy"
BASE COUNT 11 a 8 c 20 g 14 t
ORIGIN

Query Match 72.0%; Score 10.8; DB 9; Length 53;
Best Local Similarity 64.3%; Pred. No. 5.8e+04;
Matches 9; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

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Qy          2 GAUAACGUGAAGAU 15
              ||:|| |:| |||:
Db         27 GATAAGGTGCAGAT 40
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Search completed: July 6, 2003, 15:28:26
Job time : 1011.73 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: July 6, 2003, 15:04:31 ; Search time 85 Seconds
(without alignments)
275.469 Million cell updates/sec

Title: US-09-780-929-97
Perfect score: 15
Sequence: 1 agauaacgugaagau 15

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1085931 seqs, 780495707 residues

Total number of hits satisfying chosen parameters: 885896

Minimum DB seq length: 0
Maximum DB seq length: 60

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA:*
1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
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4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
9: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
10: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*
11: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
12: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:*
13: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
14: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	15	100.0	15	10	US-09-780-929-97	Sequence 97, Appl
2	15	100.0	27	10	US-09-780-929-3	Sequence 3, Appli
3	15	100.0	27	10	US-09-780-929-126	Sequence 126, App
4	15	100.0	28	10	US-09-780-929-1	Sequence 1, Appli
5	15	100.0	28	10	US-09-780-929-2	Sequence 2, Appli
6	15	100.0	28	10	US-09-780-929-4	Sequence 4, Appli
7	15	100.0	28	10	US-09-780-929-5	Sequence 5, Appli
8	15	100.0	28	10	US-09-780-929-6	Sequence 6, Appli
9	15	100.0	28	10	US-09-780-929-7	Sequence 7, Appli
10	15	100.0	28	10	US-09-780-929-8	Sequence 8, Appli
11	15	100.0	28	10	US-09-780-929-9	Sequence 9, Appli
12	15	100.0	28	10	US-09-780-929-10	Sequence 10, Appl
13	15	100.0	28	10	US-09-780-929-11	Sequence 11, Appl
14	15	100.0	28	10	US-09-780-929-12	Sequence 12, Appl
15	15	100.0	28	10	US-09-780-929-13	Sequence 13, Appl
16	15	100.0	28	10	US-09-780-929-14	Sequence 14, Appl
17	15	100.0	28	10	US-09-780-929-15	Sequence 15, Appl
18	15	100.0	28	10	US-09-780-929-16	Sequence 16, Appl
19	15	100.0	28	10	US-09-780-929-17	Sequence 17, Appl
20	15	100.0	28	10	US-09-780-929-18	Sequence 18, Appl
21	15	100.0	28	10	US-09-780-929-19	Sequence 19, Appl
22	15	100.0	28	10	US-09-780-929-20	Sequence 20, Appl
23	15	100.0	28	10	US-09-780-929-21	Sequence 21, Appl
24	15	100.0	28	10	US-09-780-929-22	Sequence 22, Appl
25	15	100.0	28	10	US-09-780-929-23	Sequence 23, Appl
26	15	100.0	28	10	US-09-780-929-24	Sequence 24, Appl
27	15	100.0	28	10	US-09-780-929-25	Sequence 25, Appl
28	15	100.0	28	10	US-09-780-929-26	Sequence 26, Appl
29	15	100.0	28	10	US-09-780-929-27	Sequence 27, Appl
30	15	100.0	28	10	US-09-780-929-28	Sequence 28, Appl
31	15	100.0	28	10	US-09-780-929-29	Sequence 29, Appl
32	15	100.0	28	10	US-09-780-929-30	Sequence 30, Appl
33	15	100.0	28	10	US-09-780-929-31	Sequence 31, Appl
34	15	100.0	28	10	US-09-780-929-32	Sequence 32, Appl
35	15	100.0	28	10	US-09-780-929-33	Sequence 33, Appl
36	15	100.0	28	10	US-09-780-929-34	Sequence 34, Appl
37	15	100.0	28	10	US-09-780-929-35	Sequence 35, Appl
38	15	100.0	28	10	US-09-780-929-36	Sequence 36, Appl
39	15	100.0	28	10	US-09-780-929-37	Sequence 37, Appl
40	15	100.0	28	10	US-09-780-929-38	Sequence 38, Appl
41	15	100.0	28	10	US-09-780-929-39	Sequence 39, Appl
42	15	100.0	28	10	US-09-780-929-40	Sequence 40, Appl
43	15	100.0	28	10	US-09-780-929-41	Sequence 41, Appl
44	15	100.0	28	10	US-09-780-929-42	Sequence 42, Appl
45	15	100.0	28	10	US-09-780-929-43	Sequence 43, Appl

ALIGNMENTS

RESULT 1
US-09-780-929-97
; Sequence 97, Application US/09780929
; Patent No. US20020151693A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc
; APPLICANT: Breaker, Ronald
; APPLICANT: Beigelman, Leo
; TITLE OF INVENTION: Nucleic Acid Catalysts with Endonuclease Activity
; FILE REFERENCE: MBHB00-884-H (500/001)
; CURRENT APPLICATION NUMBER: US/09/780,929
; CURRENT FILING DATE: 2001-02-08
; PRIOR APPLICATION NUMBER: US 60/181,360
; PRIOR FILING DATE: 2000-02-08
; NUMBER OF SEQ ID NOS: 126
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 97
; LENGTH: 15
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-09-780-929-97

Query Match 100.0%; Score 15; DB 10; Length 15;
Best Local Similarity 100.0%; Pred. No. 87;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGAUAACGUGAAGAU 15
|||||||||||||||
Db 1 AGAUAACGUGAAGAU 15

RESULT 2
US-09-780-929-3
; Sequence 3, Application US/09780929
; Patent No. US20020151693A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc
; APPLICANT: Breaker, Ronald
; APPLICANT: Beigelman, Leo
; TITLE OF INVENTION: Nucleic Acid Catalysts with Endonuclease Activity

; FILE REFERENCE: MBHB00-884-H (500/001)
; CURRENT APPLICATION NUMBER: US/09/780,929
; CURRENT FILING DATE: 2001-02-08
; PRIOR APPLICATION NUMBER: US 60/181,360
; PRIOR FILING DATE: 2000-02-08
; NUMBER OF SEQ ID NOS: 126
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 27
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-09-780-929-3

Query Match 100.0%; Score 15; DB 10; Length 27;
Best Local Similarity 100.0%; Pred. No. 90;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGAUAACGUGAAGAU 15
||||||||||||||||
Db 7 AGAUAACGUGAAGAU 21

RESULT 3
US-09-780-929-126
; Sequence 126, Application US/09780929
; Patent No. US20020151693A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc
; APPLICANT: Breaker, Ronald
; APPLICANT: Beigelman, Leo
; TITLE OF INVENTION: Nucleic Acid Catalysts with Endonuclease Activity
; FILE REFERENCE: MBHB00-884-H (500/001)
; CURRENT APPLICATION NUMBER: US/09/780,929
; CURRENT FILING DATE: 2001-02-08
; PRIOR APPLICATION NUMBER: US 60/181,360
; PRIOR FILING DATE: 2000-02-08
; NUMBER OF SEQ ID NOS: 126
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 126
; LENGTH: 27
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
; NAME/KEY: misc_feature
; LOCATION: (1)..(6)
; OTHER INFORMATION: 2'-O-Methyl
; NAME/KEY: misc_feature
; LOCATION: (21)..(27)
; OTHER INFORMATION: 2'-O-Methyl
US-09-780-929-126

Query Match 100.0%; Score 15; DB 10; Length 27;
Best Local Similarity 100.0%; Pred. No. 90;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGAUAACGUGAAGAU 15
||||||||||||||||
Db 7 AGAUAACGUGAAGAU 21

RESULT 4
US-09-780-929-1
; Sequence 1, Application US/09780929
; Patent No. US20020151693A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc
; APPLICANT: Breaker, Ronald
; APPLICANT: Beigelman, Leo
; TITLE OF INVENTION: Nucleic Acid Catalysts with Endonuclease Activity
; FILE REFERENCE: MBHB00-884-H (500/001)
; CURRENT APPLICATION NUMBER: US/09/780,929
; CURRENT FILING DATE: 2001-02-08
; PRIOR APPLICATION NUMBER: US 60/181,360
; PRIOR FILING DATE: 2000-02-08
; NUMBER OF SEQ ID NOS: 126
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 28
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
; NAME/KEY: misc_feature
; LOCATION: (1)..(6)
; OTHER INFORMATION: 2'-O-Methyl
; NAME/KEY: misc_feature
; LOCATION: (21)..(27)
; OTHER INFORMATION: 2'-O-Methyl
; NAME/KEY: misc_feature
; LOCATION: (28)..(28)
; OTHER INFORMATION: n stands for inverted deoxyabasic derivative
US-09-780-929-1

Query Match 100.0%; Score 15; DB 10; Length 28;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGAUAACGUGAAGAU 15
||||||||||||||||
Db 7 AGAUAACGUGAAGAU 21

RESULT 5
US-09-780-929-2
; Sequence 2, Application US/09780929
; Patent No. US20020151693A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc
; APPLICANT: Breaker, Ronald
; APPLICANT: Beigelman, Leo
; TITLE OF INVENTION: Nucleic Acid Catalysts with Endonuclease Activity
; FILE REFERENCE: MBHB00-884-H (500/001)
; CURRENT APPLICATION NUMBER: US/09/780,929
; CURRENT FILING DATE: 2001-02-08
; PRIOR APPLICATION NUMBER: US 60/181,360
; PRIOR FILING DATE: 2000-02-08
; NUMBER OF SEQ ID NOS: 126
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 28
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
; NAME/KEY: misc_feature
; LOCATION: (1)..(5)
; OTHER INFORMATION: 2'-O-Methyl
; NAME/KEY: misc_feature
; LOCATION: (21)..(27)
; OTHER INFORMATION: 2'-O-Methyl
; NAME/KEY: misc_feature
; LOCATION: (28)..(28)
; OTHER INFORMATION: n stands for inverted deoxyabasic derivative
US-09-780-929-2

Query Match 100.0%; Score 15; DB 10; Length 28;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGAUAACGUGAAGAU 15
||||||||||||||||
Db 7 AGAUAACGUGAAGAU 21

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RESULT 6
US-09-780-929-4
; Sequence 4, Application US/09780929
; Patent No. US20020151693A1
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals, Inc
;  APPLICANT:  Breaker, Ronald
;  APPLICANT:  Beigelman, Leo
;  TITLE OF INVENTION: Nucleic Acid Catalysts with Endonuclease Activity
;  FILE REFERENCE: MBHB00-884-H (500/001)
;  CURRENT APPLICATION NUMBER: US/09/780,929
;  CURRENT FILING DATE:  2001-02-08
;  PRIOR APPLICATION NUMBER: US 60/181,360
;  PRIOR FILING DATE: 2000-02-08
;  NUMBER OF SEQ ID NOS: 126
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
;   LENGTH: 28
;   TYPE: RNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  Enzymatic Nucleic Acid
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(5)
;   OTHER INFORMATION: 2'-O-Methyl
;   NAME/KEY: misc_feature
;   LOCATION: (22)..(27)
;   OTHER INFORMATION: 2'-O-Methyl
;   NAME/KEY: misc_feature
;   LOCATION: (28)..(28)
;   OTHER INFORMATION: n stands for inverted deoxyabasic derivative
US-09-780-929-4

  Query Match            100.0%;  Score 15;  DB 10;  Length 28;
  Best Local Similarity   100.0%;  Pred. No. 91;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAUAACGUGAAGAU 15
              |||||||||||||||
Db          7 AGAUAACGUGAAGAU 21


RESULT 7
US-09-780-929-5
; Sequence 5, Application US/09780929
; Patent No. US20020151693A1
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals, Inc
;  APPLICANT:  Breaker, Ronald
;  APPLICANT:  Beigelman, Leo
;  TITLE OF INVENTION: Nucleic Acid Catalysts with Endonuclease Activity
;  FILE REFERENCE: MBHB00-884-H (500/001)
;  CURRENT APPLICATION NUMBER: US/09/780,929
;  CURRENT FILING DATE:  2001-02-08
;  PRIOR APPLICATION NUMBER: US 60/181,360
;  PRIOR FILING DATE: 2000-02-08
;  NUMBER OF SEQ ID NOS: 126
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
;   LENGTH: 28
;   TYPE: RNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  Enzymatic Nucleic Acid
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(5)
;   OTHER INFORMATION: 2'-O-Methyl
;   NAME/KEY: misc_feature
;   LOCATION: (23)..(27)
;   OTHER INFORMATION: 2'-O-Methyl
;   NAME/KEY: misc_feature
;   LOCATION: (28)..(28)
;   OTHER INFORMATION: n stands for inverted deoxyabasic derivative
US-09-780-929-5

  Query Match            100.0%;  Score 15;  DB 10;  Length 28;
  Best Local Similarity   100.0%;  Pred. No. 91;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAUAACGUGAAGAU 15
              |||||||||||||||
Db          7 AGAUAACGUGAAGAU 21


RESULT 8
US-09-780-929-6
; Sequence 6, Application US/09780929
; Patent No. US20020151693A1
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals, Inc
;  APPLICANT:  Breaker, Ronald
;  APPLICANT:  Beigelman, Leo
;  TITLE OF INVENTION: Nucleic Acid Catalysts with Endonuclease Activity
;  FILE REFERENCE: MBHB00-884-H (500/001)
;  CURRENT APPLICATION NUMBER: US/09/780,929
;  CURRENT FILING DATE:  2001-02-08
;  PRIOR APPLICATION NUMBER: US 60/181,360
;  PRIOR FILING DATE: 2000-02-08
;  NUMBER OF SEQ ID NOS: 126
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
;   LENGTH: 28
;   TYPE: RNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  Enzymatic Nucleic Acid
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(4)
;   OTHER INFORMATION: 2'-O-Methyl
;   NAME/KEY: misc_feature
;   LOCATION: (24)..(27)
;   OTHER INFORMATION: 2'-O-Methyl
;   NAME/KEY: misc_feature
;   LOCATION: (28)..(28)
;   OTHER INFORMATION: n stands for inverted deoxyabasic derivative
US-09-780-929-6

  Query Match            100.0%;  Score 15;  DB 10;  Length 28;
  Best Local Similarity   100.0%;  Pred. No. 91;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAUAACGUGAAGAU 15
              |||||||||||||||
Db          7 AGAUAACGUGAAGAU 21


RESULT 9
US-09-780-929-7
; Sequence 7, Application US/09780929
; Patent No. US20020151693A1
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals, Inc
;  APPLICANT:  Breaker, Ronald
;  APPLICANT:  Beigelman, Leo
;  TITLE OF INVENTION: Nucleic Acid Catalysts with Endonuclease Activity
;  FILE REFERENCE: MBHB00-884-H (500/001)
;  CURRENT APPLICATION NUMBER: US/09/780,929
;  CURRENT FILING DATE:  2001-02-08
;  PRIOR APPLICATION NUMBER: US 60/181,360
;  PRIOR FILING DATE: 2000-02-08
;  NUMBER OF SEQ ID NOS: 126
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7
;   LENGTH: 28
;   TYPE: RNA
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;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  Enzymatic Nucleic Acid
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(4)
;   OTHER INFORMATION: 2'-O-Methyl
;   NAME/KEY: misc_feature
;   LOCATION: (23)..(27)
;   OTHER INFORMATION: 2'-O-Methyl
;   NAME/KEY: misc_feature
;   LOCATION: (28)..(28)
;   OTHER INFORMATION: n stands for inverted deoxyabasic derivative
US-09-780-929-7

  Query Match             100.0%;  Score 15;  DB 10;  Length 28;
  Best Local Similarity   100.0%;  Pred. No. 91;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAUAACGUGAAGAU 15
              |||||||||||||||
Db          7 AGAUAACGUGAAGAU 21


RESULT 10
US-09-780-929-8
; Sequence 8, Application US/09780929
; Patent No. US20020151693A1
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals, Inc
;  APPLICANT:  Breaker, Ronald
;  APPLICANT:  Beigelman, Leo
;  TITLE OF INVENTION: Nucleic Acid Catalysts with Endonuclease Activity
;  FILE REFERENCE: MBHB00-884-H (500/001)
;  CURRENT APPLICATION NUMBER: US/09/780,929
;  CURRENT FILING DATE:  2001-02-08
;  PRIOR APPLICATION NUMBER: US 60/181,360
;  PRIOR FILING DATE: 2000-02-08
;  NUMBER OF SEQ ID NOS: 126
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8
;   LENGTH: 28
;   TYPE: RNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  Enzymatic Nucleic Acid
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(6)
;   OTHER INFORMATION: 2'-O-Methyl
;   NAME/KEY: misc_feature
;   LOCATION: (20)..(27)
;   OTHER INFORMATION: 2'-O-Methyl
;   NAME/KEY: misc_feature
;   LOCATION: (28)..(28)
;   OTHER INFORMATION: n stands for inverted deoxyabasic derivative
US-09-780-929-8

  Query Match             100.0%;  Score 15;  DB 10;  Length 28;
  Best Local Similarity   100.0%;  Pred. No. 91;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAUAACGUGAAGAU 15
              |||||||||||||||
Db          7 AGAUAACGUGAAGAU 21


RESULT 11
US-09-780-929-9
; Sequence 9, Application US/09780929
; Patent No. US20020151693A1
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals, Inc
;  APPLICANT:  Breaker, Ronald
;  APPLICANT:  Beigelman, Leo
;  TITLE OF INVENTION: Nucleic Acid Catalysts with Endonuclease Activity
;  FILE REFERENCE: MBHB00-884-H (500/001)
;  CURRENT APPLICATION NUMBER: US/09/780,929
;  CURRENT FILING DATE:  2001-02-08
;  PRIOR APPLICATION NUMBER: US 60/181,360
;  PRIOR FILING DATE: 2000-02-08
;  NUMBER OF SEQ ID NOS: 126
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 9
;   LENGTH: 28
;   TYPE: RNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  Enzymatic Nucleic Acid
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(6)
;   OTHER INFORMATION: 2'-O-Methyl
;   NAME/KEY: misc_feature
;   LOCATION: (12)..(12)
;   OTHER INFORMATION: 2'-O-Methyl
;   NAME/KEY: misc_feature
;   LOCATION: (21)..(27)
;   OTHER INFORMATION: 2'-O-Methyl
;   NAME/KEY: misc_feature
;   LOCATION: (28)..(28)
;   OTHER INFORMATION: n stands for inverted deoxyabasic derivative
US-09-780-929-9

  Query Match             100.0%;  Score 15;  DB 10;  Length 28;
  Best Local Similarity   100.0%;  Pred. No. 91;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAUAACGUGAAGAU 15
              |||||||||||||||
Db          7 AGAUAACGUGAAGAU 21


RESULT 12
US-09-780-929-10
; Sequence 10, Application US/09780929
; Patent No. US20020151693A1
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals, Inc
;  APPLICANT:  Breaker, Ronald
;  APPLICANT:  Beigelman, Leo
;  TITLE OF INVENTION: Nucleic Acid Catalysts with Endonuclease Activity
;  FILE REFERENCE: MBHB00-884-H (500/001)
;  CURRENT APPLICATION NUMBER: US/09/780,929
;  CURRENT FILING DATE:  2001-02-08
;  PRIOR APPLICATION NUMBER: US 60/181,360
;  PRIOR FILING DATE: 2000-02-08
;  NUMBER OF SEQ ID NOS: 126
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 10
;   LENGTH: 28
;   TYPE: RNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  Enzymatic Nucleic Acid
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(7)
;   OTHER INFORMATION: 2'-O-Methyl
;   NAME/KEY: misc_feature
;   LOCATION: (21)..(27)
;   OTHER INFORMATION: 2'-O-Methyl
;   NAME/KEY: misc_feature
;   LOCATION: (28)..(28)
;   OTHER INFORMATION: n stands for inverted deoxyabasic derivative
US-09-780-929-10

  Query Match             100.0%;  Score 15;  DB 10;  Length 28;
  Best Local Similarity   100.0%;  Pred. No. 91;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
```

```
Qy          1 AGAUAACGUGAAGAU 15
              |||||||||||||||
Db          7 AGAUAACGUGAAGAU 21


RESULT 13
US-09-780-929-11
; Sequence 11, Application US/09780929
; Patent No. US20020151693A1
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals, Inc
;  APPLICANT:  Breaker, Ronald
;  APPLICANT:  Beigelman, Leo
;  TITLE OF INVENTION: Nucleic Acid Catalysts with Endonuclease Activity
;  FILE REFERENCE: MBHB00-884-H (500/001)
;  CURRENT APPLICATION NUMBER: US/09/780,929
;  CURRENT FILING DATE:  2001-02-08
;  PRIOR APPLICATION NUMBER: US 60/181,360
;  PRIOR FILING DATE: 2000-02-08
;  NUMBER OF SEQ ID NOS: 126
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 11
;   LENGTH: 28
;   TYPE: RNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  Enzymatic Nucleic Acid
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(6)
;   OTHER INFORMATION: 2'-O-Methyl
;   NAME/KEY: misc_feature
;   LOCATION: (21)..(27)
;   OTHER INFORMATION: 2'-O-Methyl
;   NAME/KEY: misc_feature
;   LOCATION: (28)..(28)
;   OTHER INFORMATION: n stands for inverted deoxyabasic derivative
US-09-780-929-11

  Query Match             100.0%;  Score 15;  DB 10;  Length 28;
  Best Local Similarity   100.0%;  Pred. No. 91;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAUAACGUGAAGAU 15
              |||||||||||||||
Db          7 AGAUAACGUGAAGAU 21


RESULT 14
US-09-780-929-12
; Sequence 12, Application US/09780929
; Patent No. US20020151693A1
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals, Inc
;  APPLICANT:  Breaker, Ronald
;  APPLICANT:  Beigelman, Leo
;  TITLE OF INVENTION: Nucleic Acid Catalysts with Endonuclease Activity
;  FILE REFERENCE: MBHB00-884-H (500/001)
;  CURRENT APPLICATION NUMBER: US/09/780,929
;  CURRENT FILING DATE:  2001-02-08
;  PRIOR APPLICATION NUMBER: US 60/181,360
;  PRIOR FILING DATE: 2000-02-08
;  NUMBER OF SEQ ID NOS: 126
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 12
;   LENGTH: 28
;   TYPE: RNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  Enzymatic Nucleic Acid
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(6)
;   OTHER INFORMATION: 2'-O-Methyl
;   NAME/KEY: misc_feature
;   LOCATION: (18)..(18)
;   OTHER INFORMATION: 2'-O-Methyl
;   NAME/KEY: misc_feature
;   LOCATION: (21)..(27)
;   OTHER INFORMATION: 2'-O-Methyl
;   NAME/KEY: misc_feature
;   LOCATION: (28)..(28)
;   OTHER INFORMATION: n stands for inverted deoxyabasic derivative
US-09-780-929-12

  Query Match             100.0%;  Score 15;  DB 10;  Length 28;
  Best Local Similarity   100.0%;  Pred. No. 91;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAUAACGUGAAGAU 15
              |||||||||||||||
Db          7 AGAUAACGUGAAGAU 21


RESULT 15
US-09-780-929-13
; Sequence 13, Application US/09780929
; Patent No. US20020151693A1
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals, Inc
;  APPLICANT:  Breaker, Ronald
;  APPLICANT:  Beigelman, Leo
;  TITLE OF INVENTION: Nucleic Acid Catalysts with Endonuclease Activity
;  FILE REFERENCE: MBHB00-884-H (500/001)
;  CURRENT APPLICATION NUMBER: US/09/780,929
;  CURRENT FILING DATE:  2001-02-08
;  PRIOR APPLICATION NUMBER: US 60/181,360
;  PRIOR FILING DATE: 2000-02-08
;  NUMBER OF SEQ ID NOS: 126
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 13
;   LENGTH: 28
;   TYPE: RNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  Enzymatic Nucleic Acid
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(6)
;   OTHER INFORMATION: 2'-O-Methyl
;   NAME/KEY: misc_feature
;   LOCATION: (17)..(17)
;   OTHER INFORMATION: 2'-O-Methyl
;   NAME/KEY: misc_feature
;   LOCATION: (21)..(27)
;   OTHER INFORMATION: 2'-O-Methyl
;   NAME/KEY: misc_feature
;   LOCATION: (28)..(28)
;   OTHER INFORMATION: n stands for inverted deoxyabasic derivative
US-09-780-929-13

  Query Match             100.0%;  Score 15;  DB 10;  Length 28;
  Best Local Similarity   100.0%;  Pred. No. 91;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAUAACGUGAAGAU 15
              |||||||||||||||
Db          7 AGAUAACGUGAAGAU 21


Search completed: July  6, 2003, 16:52:32
Job time : 85 secs
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: July 6, 2003, 14:40:47 ; Search time 1625.91 Seconds
(without alignments)
231.955 Million cell updates/sec

Title: US-09-780-929-97
Perfect score: 15
Sequence: 1 agauaacgugaagau 15

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 24791104 seqs, 12571243825 residues

Total number of hits satisfying chosen parameters: 12745074

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	15	100.0	27	30	US-09-780-929-3	Sequence 3, Appli
3	15	100.0	27	30	US-09-780-929-126	Sequence 126, App
4	15	100.0	28	30	US-09-780-929-1	Sequence 1, Appli
5	15	100.0	28	30	US-09-780-929-2	Sequence 2, Appli
6	15	100.0	28	30	US-09-780-929-4	Sequence 4, Appli
7	15	100.0	28	30	US-09-780-929-5	Sequence 5, Appli
8	15	100.0	28	30	US-09-780-929-6	Sequence 6, Appli
9	15	100.0	28	30	US-09-780-929-7	Sequence 7, Appli
10	15	100.0	28	30	US-09-780-929-8	Sequence 8, Appli
11	15	100.0	28	30	US-09-780-929-9	Sequence 9, Appli
12	15	100.0	28	30	US-09-780-929-10	Sequence 10, Appl
13	15	100.0	28	30	US-09-780-929-11	Sequence 11, Appl
14	15	100.0	28	30	US-09-780-929-12	Sequence 12, Appl
15	15	100.0	28	30	US-09-780-929-13	Sequence 13, Appl
16	15	100.0	28	30	US-09-780-929-14	Sequence 14, Appl
17	15	100.0	28	30	US-09-780-929-15	Sequence 15, Appl
18	15	100.0	28	30	US-09-780-929-16	Sequence 16, Appl
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21	15	100.0	28	30	US-09-780-929-19	Sequence 19, Appl

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24	15	100.0	28	30	US-09-780-929-22	Sequence 22, Appl
25	15	100.0	28	30	US-09-780-929-23	Sequence 23, Appl
26	15	100.0	28	30	US-09-780-929-24	Sequence 24, Appl
27	15	100.0	28	30	US-09-780-929-25	Sequence 25, Appl
28	15	100.0	28	30	US-09-780-929-26	Sequence 26, Appl
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42	15	100.0	28	30	US-09-780-929-40	Sequence 40, Appl
43	15	100.0	28	30	US-09-780-929-41	Sequence 41, Appl
44	15	100.0	28	30	US-09-780-929-42	Sequence 42, Appl
45	15	100.0	28	30	US-09-780-929-43	Sequence 43, Appl

ALIGNMENTS

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RESULT 1
US-09-780-929-97
; Sequence 97, Application US/09780929
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals, Inc
;  APPLICANT:  Breaker, Ronald
;  APPLICANT:  Beigelman, Leo
;  TITLE OF INVENTION: Nucleic Acid Catalysts with Endonuclease Activity
;  FILE REFERENCE: MBHB00-884-H (500/001)
;  CURRENT APPLICATION NUMBER: US/09/780,929
;  CURRENT FILING DATE:  2001-02-08
;  PRIOR APPLICATION NUMBER: US 60/181,360
;  PRIOR FILING DATE: 2000-02-08
;  NUMBER OF SEQ ID NOS: 126
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 97
;   LENGTH: 15
;   TYPE: RNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  Enzymatic Nucleic Acid
US-09-780-929-97

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Db          1 AGAUAACGUGAAGAU 15


RESULT 2
US-09-780-929-3
; Sequence 3, Application US/09780929
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals, Inc
;  APPLICANT:  Breaker, Ronald
;  APPLICANT:  Beigelman, Leo
;  TITLE OF INVENTION: Nucleic Acid Catalysts with Endonuclease Activity
;  FILE REFERENCE: MBHB00-884-H (500/001)
;  CURRENT APPLICATION NUMBER: US/09/780,929
;  CURRENT FILING DATE:  2001-02-08
;  PRIOR APPLICATION NUMBER: US 60/181,360
;  PRIOR FILING DATE: 2000-02-08
;  NUMBER OF SEQ ID NOS: 126
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
;   LENGTH: 27
;   TYPE: RNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  Enzymatic Nucleic Acid
US-09-780-929-3

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Qy          1 AGAUAACGUGAAGAU 15
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Db          7 AGAUAACGUGAAGAU 21


RESULT 3
US-09-780-929-126
; Sequence 126, Application US/09780929
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals, Inc
;  APPLICANT:  Breaker, Ronald
;  APPLICANT:  Beigelman, Leo
;  TITLE OF INVENTION: Nucleic Acid Catalysts with Endonuclease Activity
;  FILE REFERENCE: MBHB00-884-H (500/001)
;  CURRENT APPLICATION NUMBER: US/09/780,929
;  CURRENT FILING DATE:  2001-02-08
;  PRIOR APPLICATION NUMBER: US 60/181,360
;  PRIOR FILING DATE: 2000-02-08
;  NUMBER OF SEQ ID NOS: 126
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 126
;   LENGTH: 27
;   TYPE: RNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  Enzymatic Nucleic Acid
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(6)
;   OTHER INFORMATION: 2'-O-Methyl
;   NAME/KEY: misc_feature
;   LOCATION: (21)..(27)
;   OTHER INFORMATION: 2'-O-Methyl
US-09-780-929-126

  Query Match             100.0%;  Score 15;  DB 30;  Length 27;
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  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAUAACGUGAAGAU 15
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Db          7 AGAUAACGUGAAGAU 21


RESULT 4
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; Sequence 1, Application US/09780929
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals, Inc
;  APPLICANT:  Breaker, Ronald
;  APPLICANT:  Beigelman, Leo
;  TITLE OF INVENTION: Nucleic Acid Catalysts with Endonuclease Activity
;  FILE REFERENCE: MBHB00-884-H (500/001)
;  CURRENT APPLICATION NUMBER: US/09/780,929
;  CURRENT FILING DATE:  2001-02-08
;  PRIOR APPLICATION NUMBER: US 60/181,360
;  PRIOR FILING DATE: 2000-02-08
;  NUMBER OF SEQ ID NOS: 126
;  SOFTWARE: PatentIn version 3.0
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;   ORGANISM: Artificial Sequence
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;   LOCATION: (1)..(6)
;   OTHER INFORMATION: 2'-O-Methyl
;   NAME/KEY: misc_feature
;   LOCATION: (21)..(27)
;   OTHER INFORMATION: 2'-O-Methyl
;   NAME/KEY: misc_feature
;   LOCATION: (28)..(28)
;   OTHER INFORMATION: n stands for inverted deoxyabasic derivative
US-09-780-929-1

  Query Match            100.0%;  Score 15;  DB 30;  Length 28;
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  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAUAACGUGAAGAU 15
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Db          7 AGAUAACGUGAAGAU 21


RESULT 5
US-09-780-929-2
; Sequence 2, Application US/09780929
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals, Inc
;  APPLICANT:  Breaker, Ronald
;  APPLICANT:  Beigelman, Leo
;  TITLE OF INVENTION: Nucleic Acid Catalysts with Endonuclease Activity
;  FILE REFERENCE: MBHB00-884-H (500/001)
;  CURRENT APPLICATION NUMBER: US/09/780,929
;  CURRENT FILING DATE:  2001-02-08
;  PRIOR APPLICATION NUMBER: US 60/181,360
;  PRIOR FILING DATE: 2000-02-08
;  NUMBER OF SEQ ID NOS: 126
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; SEQ ID NO 2
;   LENGTH: 28
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;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  Enzymatic Nucleic Acid
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(5)
;   OTHER INFORMATION: 2'-O-Methyl
;   NAME/KEY: misc_feature
;   LOCATION: (21)..(27)
;   OTHER INFORMATION: 2'-O-Methyl
;   NAME/KEY: misc_feature
;   LOCATION: (28)..(28)
;   OTHER INFORMATION: n stands for inverted deoxyabasic derivative
US-09-780-929-2

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  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAUAACGUGAAGAU 15
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Db          7 AGAUAACGUGAAGAU 21


RESULT 6
US-09-780-929-4
; Sequence 4, Application US/09780929
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals, Inc
;  APPLICANT:  Breaker, Ronald
;  APPLICANT:  Beigelman, Leo
;  TITLE OF INVENTION: Nucleic Acid Catalysts with Endonuclease Activity
;  FILE REFERENCE: MBHB00-884-H (500/001)
;  CURRENT APPLICATION NUMBER: US/09/780,929
;  CURRENT FILING DATE:  2001-02-08
;  PRIOR APPLICATION NUMBER: US 60/181,360
;  PRIOR FILING DATE: 2000-02-08
;  NUMBER OF SEQ ID NOS: 126
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
;   LENGTH: 28
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;   OTHER INFORMATION: Description of Artificial Sequence:  Enzymatic Nucleic Acid
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(5)
;   OTHER INFORMATION: 2'-O-Methyl
;   NAME/KEY: misc_feature
;   LOCATION: (22)..(27)
;   OTHER INFORMATION: 2'-O-Methyl
;   NAME/KEY: misc_feature
;   LOCATION: (28)..(28)
;   OTHER INFORMATION: n stands for inverted deoxyabasic derivative
US-09-780-929-4

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  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAUAACGUGAAGAU 15
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Db          7 AGAUAACGUGAAGAU 21


RESULT 7
US-09-780-929-5
; Sequence 5, Application US/09780929
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals, Inc
;  APPLICANT:  Breaker, Ronald
;  APPLICANT:  Beigelman, Leo
;  TITLE OF INVENTION: Nucleic Acid Catalysts with Endonuclease Activity
;  FILE REFERENCE: MBHB00-884-H (500/001)
;  CURRENT APPLICATION NUMBER: US/09/780,929
;  CURRENT FILING DATE:  2001-02-08
;  PRIOR APPLICATION NUMBER: US 60/181,360
;  PRIOR FILING DATE: 2000-02-08
;  NUMBER OF SEQ ID NOS: 126
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
;   LENGTH: 28
;   TYPE: RNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  Enzymatic Nucleic Acid
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(5)
;   OTHER INFORMATION: 2'-O-Methyl
;   NAME/KEY: misc_feature
;   LOCATION: (23)..(27)
;   OTHER INFORMATION: 2'-O-Methyl
;   NAME/KEY: misc_feature
;   LOCATION: (28)..(28)
;   OTHER INFORMATION: n stands for inverted deoxyabasic derivative
US-09-780-929-5

  Query Match            100.0%;  Score 15;  DB 30;  Length 28;
  Best Local Similarity   100.0%;  Pred. No. 4.2e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAUAACGUGAAGAU 15
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Db          7 AGAUAACGUGAAGAU 21


RESULT 8
US-09-780-929-6
; Sequence 6, Application US/09780929
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals, Inc
;  APPLICANT:  Breaker, Ronald
;  APPLICANT:  Beigelman, Leo
;  TITLE OF INVENTION: Nucleic Acid Catalysts with Endonuclease Activity
;  FILE REFERENCE: MBHB00-884-H (500/001)
;  CURRENT APPLICATION NUMBER: US/09/780,929
;  CURRENT FILING DATE:  2001-02-08
;  PRIOR APPLICATION NUMBER: US 60/181,360
;  PRIOR FILING DATE: 2000-02-08
;  NUMBER OF SEQ ID NOS: 126
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;   NAME/KEY: misc_feature
;   LOCATION: (28)..(28)
;   OTHER INFORMATION: n stands for inverted deoxyabasic derivative
US-09-780-929-6

  Query Match             100.0%;  Score 15;  DB 30;  Length 28;
  Best Local Similarity   100.0%;  Pred. No. 4.2e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAUAACGUGAAGAU 15
              |||||||||||||||
Db          7 AGAUAACGUGAAGAU 21


RESULT 9
US-09-780-929-7
; Sequence 7, Application US/09780929
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals, Inc
;  APPLICANT:  Breaker, Ronald
;  APPLICANT:  Beigelman, Leo
;  TITLE OF INVENTION: Nucleic Acid Catalysts with Endonuclease Activity
;  FILE REFERENCE: MBHB00-884-H (500/001)
;  CURRENT APPLICATION NUMBER: US/09/780,929
;  CURRENT FILING DATE:  2001-02-08
;  PRIOR APPLICATION NUMBER: US 60/181,360
;  PRIOR FILING DATE: 2000-02-08
;  NUMBER OF SEQ ID NOS: 126
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7
;   LENGTH: 28
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;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  Enzymatic Nucleic Acid
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(4)
;   OTHER INFORMATION: 2'-O-Methyl
;   NAME/KEY: misc_feature
;   LOCATION: (23)..(27)
;   OTHER INFORMATION: 2'-O-Methyl
;   NAME/KEY: misc_feature
;   LOCATION: (28)..(28)
;   OTHER INFORMATION: n stands for inverted deoxyabasic derivative
US-09-780-929-7

  Query Match             100.0%;  Score 15;  DB 30;  Length 28;
  Best Local Similarity   100.0%;  Pred. No. 4.2e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAUAACGUGAAGAU 15
              |||||||||||||||
Db          7 AGAUAACGUGAAGAU 21


RESULT 10
US-09-780-929-8
; Sequence 8, Application US/09780929
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals, Inc
;  APPLICANT:  Breaker, Ronald
;  APPLICANT:  Beigelman, Leo
;  TITLE OF INVENTION: Nucleic Acid Catalysts with Endonuclease Activity
;  FILE REFERENCE: MBHB00-884-H (500/001)
;  CURRENT APPLICATION NUMBER: US/09/780,929
;  CURRENT FILING DATE:  2001-02-08
;  PRIOR APPLICATION NUMBER: US 60/181,360
;  PRIOR FILING DATE: 2000-02-08
;  NUMBER OF SEQ ID NOS: 126
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8
;   LENGTH: 28
;   TYPE: RNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  Enzymatic Nucleic Acid
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(6)
;   OTHER INFORMATION: 2'-O-Methyl
;   NAME/KEY: misc_feature
;   LOCATION: (20)..(27)
;   OTHER INFORMATION: 2'-O-Methyl
;   NAME/KEY: misc_feature
;   LOCATION: (28)..(28)
;   OTHER INFORMATION: n stands for inverted deoxyabasic derivative
US-09-780-929-8

  Query Match             100.0%;  Score 15;  DB 30;  Length 28;
  Best Local Similarity   100.0%;  Pred. No. 4.2e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAUAACGUGAAGAU 15
              |||||||||||||||
Db          7 AGAUAACGUGAAGAU 21


RESULT 11
US-09-780-929-9
; Sequence 9, Application US/09780929
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals, Inc
;  APPLICANT:  Breaker, Ronald
;  APPLICANT:  Beigelman, Leo
;  TITLE OF INVENTION: Nucleic Acid Catalysts with Endonuclease Activity
;  FILE REFERENCE: MBHB00-884-H (500/001)
;  CURRENT APPLICATION NUMBER: US/09/780,929
;  CURRENT FILING DATE:  2001-02-08
;  PRIOR APPLICATION NUMBER: US 60/181,360
;  PRIOR FILING DATE: 2000-02-08
;  NUMBER OF SEQ ID NOS: 126
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 9
;   LENGTH: 28
;   TYPE: RNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
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;   OTHER INFORMATION: Description of Artificial Sequence:  Enzymatic Nucleic Acid
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(6)
;   OTHER INFORMATION: 2'-O-Methyl
;   NAME/KEY: misc_feature
;   LOCATION: (12)..(12)
;   OTHER INFORMATION: 2'-O-Methyl
;   NAME/KEY: misc_feature
;   LOCATION: (21)..(27)
;   OTHER INFORMATION: 2'-O-Methyl
;   NAME/KEY: misc_feature
;   LOCATION: (28)..(28)
;   OTHER INFORMATION: n stands for inverted deoxyabasic derivative
US-09-780-929-9

  Query Match           100.0%;  Score 15;  DB 30;  Length 28;
  Best Local Similarity  100.0%;  Pred. No. 4.2e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAUAACGUGAAGAU 15
              |||||||||||||||
Db          7 AGAUAACGUGAAGAU 21


RESULT 12
US-09-780-929-10
; Sequence 10, Application US/09780929
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals, Inc
;  APPLICANT:  Breaker, Ronald
;  APPLICANT:  Beigelman, Leo
;  TITLE OF INVENTION: Nucleic Acid Catalysts with Endonuclease Activity
;  FILE REFERENCE: MBHB00-884-H (500/001)
;  CURRENT APPLICATION NUMBER: US/09/780,929
;  CURRENT FILING DATE:  2001-02-08
;  PRIOR APPLICATION NUMBER: US 60/181,360
;  PRIOR FILING DATE: 2000-02-08
;  NUMBER OF SEQ ID NOS: 126
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 10
;   LENGTH: 28
;   TYPE: RNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  Enzymatic Nucleic Acid
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(7)
;   OTHER INFORMATION: 2'-O-Methyl
;   NAME/KEY: misc_feature
;   LOCATION: (21)..(27)
;   OTHER INFORMATION: 2'-O-Methyl
;   NAME/KEY: misc_feature
;   LOCATION: (28)..(28)
;   OTHER INFORMATION: n stands for inverted deoxyabasic derivative
US-09-780-929-10

  Query Match           100.0%;  Score 15;  DB 30;  Length 28;
  Best Local Similarity  100.0%;  Pred. No. 4.2e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAUAACGUGAAGAU 15
              |||||||||||||||
Db          7 AGAUAACGUGAAGAU 21


RESULT 13
US-09-780-929-11
; Sequence 11, Application US/09780929
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals, Inc
;  APPLICANT:  Breaker, Ronald
;  APPLICANT:  Beigelman, Leo
;  TITLE OF INVENTION: Nucleic Acid Catalysts with Endonuclease Activity
;  FILE REFERENCE: MBHB00-884-H (500/001)
;  CURRENT APPLICATION NUMBER: US/09/780,929
;  CURRENT FILING DATE:  2001-02-08
;  PRIOR APPLICATION NUMBER: US 60/181,360
;  PRIOR FILING DATE: 2000-02-08
;  NUMBER OF SEQ ID NOS: 126
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 11
;   LENGTH: 28
;   TYPE: RNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  Enzymatic Nucleic Acid
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(6)
;   OTHER INFORMATION: 2'-O-Methyl
;   NAME/KEY: misc_feature
;   LOCATION: (21)..(27)
;   OTHER INFORMATION: 2'-O-Methyl
;   NAME/KEY: misc_feature
;   LOCATION: (28)..(28)
;   OTHER INFORMATION: n stands for inverted deoxyabasic derivative
US-09-780-929-11

  Query Match           100.0%;  Score 15;  DB 30;  Length 28;
  Best Local Similarity  100.0%;  Pred. No. 4.2e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAUAACGUGAAGAU 15
              |||||||||||||||
Db          7 AGAUAACGUGAAGAU 21


RESULT 14
US-09-780-929-12
; Sequence 12, Application US/09780929
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals, Inc
;  APPLICANT:  Breaker, Ronald
;  APPLICANT:  Beigelman, Leo
;  TITLE OF INVENTION: Nucleic Acid Catalysts with Endonuclease Activity
;  FILE REFERENCE: MBHB00-884-H (500/001)
;  CURRENT APPLICATION NUMBER: US/09/780,929
;  CURRENT FILING DATE:  2001-02-08
;  PRIOR APPLICATION NUMBER: US 60/181,360
;  PRIOR FILING DATE: 2000-02-08
;  NUMBER OF SEQ ID NOS: 126
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 12
;   LENGTH: 28
;   TYPE: RNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  Enzymatic Nucleic Acid
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(6)
;   OTHER INFORMATION: 2'-O-Methyl
;   NAME/KEY: misc_feature
;   LOCATION: (18)..(18)
;   OTHER INFORMATION: 2'-O-Methyl
;   NAME/KEY: misc_feature
;   LOCATION: (21)..(27)
;   OTHER INFORMATION: 2'-O-Methyl
;   NAME/KEY: misc_feature
;   LOCATION: (28)..(28)
;   OTHER INFORMATION: n stands for inverted deoxyabasic derivative
US-09-780-929-12

  Query Match           100.0%;  Score 15;  DB 30;  Length 28;
  Best Local Similarity  100.0%;  Pred. No. 4.2e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAUAACGUGAAGAU 15
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              ||||||||||||||||
Db          7 AGAUAACGUGAAGAU 21


RESULT 15
US-09-780-929-13
; Sequence 13, Application US/09780929
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals, Inc
;  APPLICANT:  Breaker, Ronald
;  APPLICANT:  Beigelman, Leo
;  TITLE OF INVENTION: Nucleic Acid Catalysts with Endonuclease Activity
;  FILE REFERENCE: MBHB00-884-H (500/001)
;  CURRENT APPLICATION NUMBER: US/09/780,929
;  CURRENT FILING DATE:  2001-02-08
;  PRIOR APPLICATION NUMBER: US 60/181,360
;  PRIOR FILING DATE: 2000-02-08
;  NUMBER OF SEQ ID NOS: 126
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 13
;   LENGTH: 28
;   TYPE: RNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  Enzymatic Nucleic Acid
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(6)
;   OTHER INFORMATION: 2'-O-Methyl
;   NAME/KEY: misc_feature
;   LOCATION: (17)..(17)
;   OTHER INFORMATION: 2'-O-Methyl
;   NAME/KEY: misc_feature
;   LOCATION: (21)..(27)
;   OTHER INFORMATION: 2'-O-Methyl
;   NAME/KEY: misc_feature
;   LOCATION: (28)..(28)
;   OTHER INFORMATION: n stands for inverted deoxyabasic derivative
US-09-780-929-13

  Query Match             100.0%;  Score 15;  DB 30;  Length 28;
  Best Local Similarity   100.0%;  Pred. No. 4.2e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAUAACGUGAAGAU 15
              ||||||||||||||||
Db          7 AGAUAACGUGAAGAU 21


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Job time : 1625.91 secs
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: July 6, 2003, 14:26:16 ; Search time 591.818 Seconds
(without alignments)
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Title: US-09-780-929-98
Perfect score: 18
Sequence: 1 aauggccuaucggugcga 18

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 897812

Minimum DB seq length: 0
Maximum DB seq length: 60

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: gb_htg:*
3: gb_in:*
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9: gb_pr:*
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33: em_htg_mus:*
34: em_htg_pln:*
35: em_htg_rod:*
36: em_htg_mam:*
37: em_htg_vrt:*
38: em_sy:*
39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	18	100.0	18	6	AX214296	AX214296 Sequence
2	18	100.0	29	6	AX214316	AX214316 Sequence
3	12.8	71.1	20	6	AX295903	AX295903 Sequence
4	12.8	71.1	24	6	AX291270	AX291270 Sequence
5	12.2	67.8	20	6	AX293899	AX293899 Sequence
6	12.2	67.8	24	6	AX289266	AX289266 Sequence
c 7	12.2	67.8	29	6	AR198859	AR198859 Sequence
8	12	66.7	22	6	AX297915	AX297915 Sequence
9	11.8	65.6	20	6	AX293092	AX293092 Sequence
c 10	11.8	65.6	20	6	E30812	E30812 Novel prote
11	11.8	65.6	22	6	AX019596	AX019596 Sequence
12	11.8	65.6	24	6	AX288459	AX288459 Sequence
13	11.8	65.6	24	6	AX447444	AX447444 Sequence
14	11.8	65.6	30	6	A29209	A29209 DNA probe f
15	11.8	65.6	30	6	A29212	A29212 Oligonucleo
16	11.8	65.6	40	6	AR178716	AR178716 Sequence
17	11.8	65.6	40	6	AR205421	AR205421 Sequence
c 18	11.6	64.4	22	6	AX166857	AX166857 Sequence
c 19	11.6	64.4	24	6	AX166856	AX166856 Sequence
c 20	11.6	64.4	25	6	AX166855	AX166855 Sequence
21	11.6	64.4	26	6	I22031	I22031 Sequence 5
c 22	11.6	64.4	29	6	AR023454	AR023454 Sequence
c 23	11.6	64.4	29	6	E46848	E46848 Derivative
c 24	11.6	64.4	30	6	AR023453	AR023453 Sequence
c 25	11.6	64.4	30	6	AR092568	AR092568 Sequence
c 26	11.6	64.4	30	6	AR139964	AR139964 Sequence
c 27	11.6	64.4	30	6	AR140283	AR140283 Sequence
c 28	11.6	64.4	30	6	AR140561	AR140561 Sequence
c 29	11.6	64.4	30	6	E46847	E46847 Derivative
30	11.6	64.4	41	6	A63966	A63966 Sequence 10
31	11.6	64.4	41	6	AR091476	AR091476 Sequence
c 32	11.6	64.4	46	6	AR170886	AR170886 Sequence
c 33	11.6	64.4	47	6	AX378262	AX378262 Sequence
34	11.4	63.3	17	6	AR057682	AR057682 Sequence
35	11.4	63.3	17	6	AR057773	AR057773 Sequence
36	11.4	63.3	17	6	AR115440	AR115440 Sequence
37	11.4	63.3	17	6	AR115531	AR115531 Sequence
38	11.4	63.3	21	6	AR167007	AR167007 Sequence
39	11.4	63.3	21	6	AR210662	AR210662 Sequence
c 40	11.4	63.3	24	6	AX447141	AX447141 Sequence
41	11.4	63.3	25	6	AR097506	AR097506 Sequence
42	11.4	63.3	25	6	AR139820	AR139820 Sequence
43	11.4	63.3	25	6	AR140127	AR140127 Sequence
44	11.4	63.3	25	6	AR142844	AR142844 Sequence
c 45	11.4	63.3	31	6	AX425973	AX425973 Sequence

ALIGNMENTS

RESULT 1
AX214296
LOCUS AX214296 18 bp mRNA linear PAT 06-SEP-2001
DEFINITION Sequence 109 from Patent WO0159102.
ACCESSION AX214296
VERSION AX214296.1 GI:15524373
KEYWORDS .
SOURCE synthetic construct.
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 18)
AUTHORS Breaker,R. and Emilsson,G.
TITLE Nucleozymes with endonuclease activity
JOURNAL Patent: WO 0159102-A 109 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; Yale University (US)

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FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="Nucleic Acid"
BASE COUNT        4 a      4 c      6 g      4 t
ORIGIN

  Query Match             100.0%;  Score 18;  DB 6;  Length 18;
  Best Local Similarity   77.8%;  Pred. No. 29;
  Matches   14;  Conservative    4;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AAUGGCCUAUCGGUGCGA 18
              ||:||||:|:|||:||||
Db          1 AATGGCCTATCGGTGCGA 18


RESULT 2
AX214316
LOCUS       AX214316                 29 bp    mRNA    linear   PAT 06-SEP-2001
DEFINITION  Sequence 129 from Patent WO0159102.
ACCESSION   AX214316
VERSION     AX214316.1  GI:15524393
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 29)
  AUTHORS   Breaker,R. and Emilsson,G.
  TITLE     Nucleozymes with endonuclease activity
  JOURNAL   Patent: WO 0159102-A 129 16-AUG-2001;
            RIBOZYME PHARMACEUTICALS, INC. (US) ; Yale University (US)
FEATURES             Location/Qualifiers
     source          1. .29
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="Nucleic Acid"
BASE COUNT        6 a      7 c     11 g      5 t
ORIGIN

  Query Match             100.0%;  Score 18;  DB 6;  Length 29;
  Best Local Similarity   77.8%;  Pred. No. 29;
  Matches   14;  Conservative    4;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AAUGGCCUAUCGGUGCGA 18
              ||:||||:|:|||:||||
Db          8 AATGGCCTATCGGTGCGA 25


RESULT 3
AX295903
LOCUS       AX295903                 20 bp    DNA     linear   PAT 21-NOV-2001
DEFINITION  Sequence 7665 from Patent WO0179548.
ACCESSION   AX295903
VERSION     AX295903.1  GI:17057592
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Barany,F., Zirvi,M., Gerry,N.P., Favis,R. and Kliman,R.
  TITLE     Method of designing addressable array for detection of nucleic acid
            sequence differences using ligase detection reaction
  JOURNAL   Patent: WO 0179548-A 7665 25-OCT-2001;
            CORNELL RESEARCH FOUNDATION, INC. (US)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="Hypothetical Probe Sequence"
BASE COUNT        2 a      6 c      6 g      6 t
ORIGIN

  Query Match             71.1%;  Score 12.8;  DB 6;  Length 20;
  Best Local Similarity   68.8%;  Pred. No. 2.5e+04;
  Matches   11;  Conservative    3;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 AUGGCCUAUCGGUGCG 17
              | ||| :|:|||:|||
Db          2 ACGGCTTATCGGTGCG 17


RESULT 4
AX291270
LOCUS       AX291270                 24 bp    DNA     linear   PAT 21-NOV-2001
DEFINITION  Sequence 3032 from Patent WO0179548.
ACCESSION   AX291270
VERSION     AX291270.1  GI:17052953
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Barany,F., Zirvi,M., Gerry,N.P., Favis,R. and Kliman,R.
  TITLE     Method of designing addressable array for detection of nucleic acid
            sequence differences using ligase detection reaction
  JOURNAL   Patent: WO 0179548-A 3032 25-OCT-2001;
            CORNELL RESEARCH FOUNDATION, INC. (US)
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="Hypothetical Probe Sequence"
BASE COUNT        2 a      7 c      7 g      8 t
ORIGIN

  Query Match             71.1%;  Score 12.8;  DB 6;  Length 24;
  Best Local Similarity   68.8%;  Pred. No. 2.5e+04;
  Matches   11;  Conservative    3;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 AUGGCCUAUCGGUGCG 17
              | ||| :|:|||:|||
Db          2 ACGGCTTATCGGTGCG 17


RESULT 5
AX293899
LOCUS       AX293899                 20 bp    DNA     linear   PAT 21-NOV-2001
DEFINITION  Sequence 5661 from Patent WO0179548.
ACCESSION   AX293899
VERSION     AX293899.1  GI:17055582
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences..
REFERENCE   1
  AUTHORS   Barany,F., Zirvi,M., Gerry,N.P., Favis,R. and Kliman,R.
  TITLE     Method of designing addressable array for detection of nucleic acid
            sequence differences using ligase detection reaction
  JOURNAL   Patent: WO 0179548-A 5661 25-OCT-2001;
            CORNELL RESEARCH FOUNDATION, INC. (US)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="Hypothetical Probe Sequence"
BASE COUNT        7 a      6 c      4 g      3 t
ORIGIN

  Query Match             67.8%;  Score 12.2;  DB 6;  Length 20;
  Best Local Similarity   64.7%;  Pred. No. 5.5e+04;
  Matches   11;  Conservative    3;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          2 AUGGCCUAUCGGUGCGA 18
              |:| || |:|| :||||
Db          3 ATGACCAATCGATGCGA 19
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RESULT 6
AX289266
LOCUS       AX289266                 24 bp    DNA     linear   PAT 21-NOV-2001
DEFINITION  Sequence 1028 from Patent WO0179548.
ACCESSION   AX289266
VERSION     AX289266.1  GI:17050949
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Barany,F., Zirvi,M., Gerry,N.P., Favis,R. and Kliman,R.
  TITLE     Method of designing addressable array for detection of nucleic acid
            sequence differences using ligase detection reaction
  JOURNAL   Patent: WO 0179548-A 1028 25-OCT-2001;
            CORNELL RESEARCH FOUNDATION, INC. (US)
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="Hypothetical Probe Sequence"
BASE COUNT        7 a      7 c      5 g      5 t
ORIGIN

  Query Match            67.8%;  Score 12.2;  DB 6;  Length 24;
  Best Local Similarity  64.7%;  Pred. No. 5.5e+04;
  Matches   11;  Conservative    3;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          2 AUGGCCUAUCGGUGCGA 18
              |:| || |:|| :||||
Db          7 ATGACCAATCGATGCGA 23


RESULT 7
AR198859/c
LOCUS       AR198859                 29 bp    DNA     linear   PAT 20-APR-2002
DEFINITION  Sequence 144 from patent US 6355411.
ACCESSION   AR198859
VERSION     AR198859.1  GI:20248933
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 29)
  AUTHORS   Ausubel,F., Goodman,H.M., Rahme,L.G., Mahajan-Miklos,S., Tan,M.-W.,
            Cao,H., Drenkard,E. and Tsongalis,J.
  TITLE     Virulence-associated nucleic acid sequences and uses thereof
  JOURNAL   Patent: US 6355411-A 144 12-MAR-2002;
FEATURES             Location/Qualifiers
     source          1. .29
                     /organism="unknown"
BASE COUNT        6 a     10 c      8 g      5 t
ORIGIN

  Query Match            67.8%;  Score 12.2;  DB 6;  Length 29;
  Best Local Similarity  64.7%;  Pred. No. 5.5e+04;
  Matches   11;  Conservative    3;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 AAUGGCCUAUCGGUGCG 17
              || ||| :|:|| :|||
Db         19 AACGGCGTATCGTTGCG 3


RESULT 8
AX297915
LOCUS       AX297915                 22 bp    DNA     linear   PAT 26-NOV-2001
DEFINITION  Sequence 4 from Patent WO0183757.
ACCESSION   AX297915
VERSION     AX297915.1  GI:17128036
KEYWORDS    .
SOURCE      TT virus.
  ORGANISM  TT virus
            Viruses; ssDNA viruses; unclassified ssDNA viruses.
REFERENCE   1
  AUTHORS   Ott,C. and Komurian-Pradel,F.
  TITLE     TT virus polypeptide, nucleic acid coding for said polypeptide and
            uses
  JOURNAL   Patent: WO 0183757-A 4 08-NOV-2001;
            BIO MERIEUX (FR)
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="TT virus"
                     /db_xref="taxon:68887"
BASE COUNT        4 a      5 c      8 g      4 t      1 others
ORIGIN

  Query Match            66.7%;  Score 12;  DB 6;  Length 22;
  Best Local Similarity  57.1%;  Pred. No. 7.1e+04;
  Matches    8;  Conservative    5;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 AUGGCCUAUCGGUG 15
              |:||||:|: |::|
Db          8 ATGGCCTATGGSTG 21


RESULT 9
AX293092
LOCUS       AX293092                 20 bp    DNA     linear   PAT 21-NOV-2001
DEFINITION  Sequence 4854 from Patent WO0179548.
ACCESSION   AX293092
VERSION     AX293092.1  GI:17054775
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Barany,F., Zirvi,M., Gerry,N.P., Favis,R. and Kliman,R.
  TITLE     Method of designing addressable array for detection of nucleic acid
            sequence differences using ligase detection reaction
  JOURNAL   Patent: WO 0179548-A 4854 25-OCT-2001;
            CORNELL RESEARCH FOUNDATION, INC. (US)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="Hypothetical Probe Sequence"
BASE COUNT        1 a      6 c      6 g      7 t
ORIGIN

  Query Match            65.6%;  Score 11.8;  DB 6;  Length 20;
  Best Local Similarity  60.0%;  Pred. No. 9.2e+04;
  Matches    9;  Conservative    4;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          3 UGGCCUAUCGGUGCG 17
              :| ||:|:| |:|||
Db          6 TGCCCTATCTGTGCG 20


RESULT 10
E30812/c
LOCUS       E30812                   20 bp    DNA     linear   PAT 18-JUN-2001
DEFINITION  Novel protein participating in differentiation of cranial nerve
            tissue cell.
ACCESSION   E30812
VERSION     E30812.1  GI:13017242
KEYWORDS    JP 1999318468-A/6.
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Shigeru,N. and Hirofumi,S.
  TITLE     Novel protein participating in differentiation of cranial nerve
            tissue cell
  JOURNAL   Patent: JP 1999318468-A 6 24-NOV-1999;
```

```
            THE KANAGAWA ACADEMY OF SCIENCE,MEIJI MILK PROD CO LTD
COMMENT     OS   Unidentified
            PN   JP 1999318468-A/6
            PD   24-NOV-1999
            PF   15-MAY-1998 JP 1998152027
            PR
            PI   SHIGERU NOGUCHI,HIROFUMI SUEMORI
            PC   C12N15/09,A01K67/027,A61K38/00,A61K48/00,C07K14/47,C07K16/18,
            PC   C12N1/19,
            PC   C12N1/21,C12N5/10,C12P21/02,C12Q1/68//(C12N5/10,C12R1:91), PC
             C12N15/00,
            PC   A61K37/02,C12N5/00,(C12N5/00,C12R1:91)
            CC   Strandedness: Single;
            CC   Topology: Linear;
            FH   Key             Location/Qualifiers
            FT   source          1. .20
            FT                   /organism='Unidentified'.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unidentified"
                     /db_xref="taxon:32644"
BASE COUNT        7 a      7 c      4 g      2 t
ORIGIN

  Query Match             65.6%;  Score 11.8;  DB 6;  Length 20;
  Best Local Similarity   60.0%;  Pred. No. 9.2e+04;
  Matches    9;  Conservative    4;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          3 UGGCCUAUCGGUGCG 17
              :|| |: :|||:|||
Db         20 TGGTCTCTCGGTGCG 6


RESULT 11
AX019596
LOCUS       AX019596                  22 bp    DNA     linear   PAT 07-SEP-2000
DEFINITION  Sequence 50 from Patent WO9938964.
ACCESSION   AX019596
VERSION     AX019596.1  GI:10043510
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Keith,W.N.
  TITLE     Promoter regions of the mouse and human telomerase rna component
            genes
  JOURNAL   Patent: WO 9938964-A 50 05-AUG-1999;
            KEITH WILLIAM NICOL (GB); CANCER RES CAMPAIGN TECH (GB)
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="Oligonucleotide"
BASE COUNT        2 a      7 c      8 g      5 t
ORIGIN

  Query Match             65.6%;  Score 11.8;  DB 6;  Length 22;
  Best Local Similarity   66.7%;  Pred. No. 9.2e+04;
  Matches   10;  Conservative    3;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          3 UGGCCUAUCGGUGCG 17
              :|||| |:| |:|||
Db          3 TGGCCAATCCGTGCG 17


RESULT 12
AX288459
LOCUS       AX288459                  24 bp    DNA     linear   PAT 21-NOV-2001
DEFINITION  Sequence 221 from Patent WO0179548.
ACCESSION   AX288459
VERSION     AX288459.1  GI:17050142
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Barany,F., Zirvi,M., Gerry,N.P., Favis,R. and Kliman,R.
  TITLE     Method of designing addressable array for detection of nucleic acid
            sequence differences using ligase detection reaction
  JOURNAL   Patent: WO 0179548-A 221 25-OCT-2001;
            CORNELL RESEARCH FOUNDATION, INC. (US)
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="Hypothetical Probe Sequence"
BASE COUNT        1 a      7 c      7 g      9 t
ORIGIN

  Query Match             65.6%;  Score 11.8;  DB 6;  Length 24;
  Best Local Similarity   60.0%;  Pred. No. 9.2e+04;
  Matches    9;  Conservative    4;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          3 UGGCCUAUCGGUGCG 17
              :| ||:|:| |:|||
Db          6 TGCCCTATCTGTGCG 20


RESULT 13
AX447444
LOCUS       AX447444                  24 bp    DNA     linear   PAT 03-JUL-2002
DEFINITION  Sequence 3899 from Patent WO0216649.
ACCESSION   AX447444
VERSION     AX447444.1  GI:21696343
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Gunderson,K.
  TITLE     Probes and decoder oligonucleotides
  JOURNAL   Patent: WO 0216649-A 3899 28-FEB-2002;
            Illumina, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="Computer Generated Probe Sequence."
BASE COUNT        6 a      6 c      8 g      4 t
ORIGIN

  Query Match             65.6%;  Score 11.8;  DB 6;  Length 24;
  Best Local Similarity   73.3%;  Pred. No. 9.2e+04;
  Matches   11;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          4 GGCCUAUCGGUGCGA 18
              ||||:|  ||:||||
Db          2 GGCCTAGAGGTGCGA 16


RESULT 14
A29209
LOCUS       A29209                    30 bp    DNA     linear   PAT 30-JUN-1995
DEFINITION  DNA probe from patent WO9111459.
ACCESSION   A29209
VERSION     A29209.1  GI:1248930
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
FEATURES             Location/Qualifiers
     source          1. .30
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
BASE COUNT        5 a      6 c     13 g      6 t
```

```
ORIGIN

  Query Match             65.6%;  Score 11.8;  DB 6;  Length 30;
  Best Local Similarity   73.3%;  Pred. No. 9.2e+04;
  Matches   11;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 AUGGCCUAUCGGUGC 16
              | ||||:| |||:||
Db          1 ACGGCCTAGCGGTGC 15


RESULT 15
A29212
LOCUS       A29212                    30 bp    DNA     linear   PAT 30-JUN-1995
DEFINITION  Oligonucleotide OAB1088 from patent WO9111459.
ACCESSION   A29212
VERSION     A29212.1  GI:1248933
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
FEATURES             Location/Qualifiers
     source          1. .30
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
BASE COUNT        5 a      6 c     13 g      6 t
ORIGIN

  Query Match             65.6%;  Score 11.8;  DB 6;  Length 30;
  Best Local Similarity   73.3%;  Pred. No. 9.2e+04;
  Matches   11;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 AUGGCCUAUCGGUGC 16
              | ||||:| |||:||
Db          1 ACGGCCTAGCGGTGC 15


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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: July 6, 2003, 14:25:15 ; Search time 193.091 Seconds
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Perfect score: 18
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 2274872

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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	18	100.0	18	22	AAS12348	DNA encoding deoxy
	2	18	100.0	29	22	AAS12381	Class IV ribozyme.
c	3	13.8	76.7	30	24	AAS19241	CMV mutagenic adap
	4	13.4	74.4	60	24	ABN47743	Human spliced tran
	5	12.8	71.1	20	24	ABI95945	Capture oligonucle
	6	12.8	71.1	24	24	ABI88460	Capture oligonucle
c	7	12.8	71.1	24	24	ABI88461	Capture oligonucle
	8	12.4	68.9	41	22	AAC87378	Staphylococcus aur
	9	12.2	67.8	20	24	ABI93941	Capture oligonucle
c	10	12.2	67.8	24	22	AAS08711	Human PD-ATP-bindi
	11	12.2	67.8	24	24	ABI84452	Capture oligonucle
c	12	12.2	67.8	24	24	ABI84453	Capture oligonucle
c	13	12.2	67.8	29	20	AAX98255	PCR primer used to
c	14	12.2	67.8	40	17	AAT70787	Stenotic carotid a
c	15	12.2	67.8	53	16	AAT21824	Human gene signatu
	16	12.2	67.8	60	24	ABN32869	Human spliced tran
	17	12	66.7	22	24	ABA04884	TT virus PCR prime
c	18	11.8	65.6	20	20	AAX94010	PCR primer used to
c	19	11.8	65.6	20	21	AAZ44197	Murine cerebral ne
	20	11.8	65.6	20	24	ABI93134	Capture oligonucle
	21	11.8	65.6	22	20	AAZ07252	Wild-type oligo h1
	22	11.8	65.6	22	20	AAZ07306	Human telomerase R
	23	11.8	65.6	24	24	ABQ03892	Oligonucleotide ad
	24	11.8	65.6	24	24	ABI82838	Capture oligonucle
c	25	11.8	65.6	24	24	ABI82839	Capture oligonucle
	26	11.8	65.6	24	24	ABI92104	Capture oligonucle
c	27	11.8	65.6	24	24	ABI92105	Capture oligonucle
	28	11.8	65.6	30	12	AAQ13310	Probe OAB 1088 for
	29	11.8	65.6	39	22	AAI68437	P.carinii 18S rRNA
	30	11.8	65.6	40	21	AAA62656	Beta-lactamase gen
c	31	11.6	64.4	22	22	AAD11273	Mycobacterium 16S
c	32	11.6	64.4	24	22	AAD11272	Mycobacterium 16S
c	33	11.6	64.4	25	22	AAD11271	Mycobacterium 16S
	34	11.6	64.4	27	19	AAV55972	Human cytokine rec
c	35	11.6	64.4	29	16	AAQ99711	Primer corresp. to
c	36	11.6	64.4	29	17	AAT10032	MDGF antisense pri
c	37	11.6	64.4	30	16	AAT04920	Mammalian stem cel
c	38	11.6	64.4	30	16	AAQ99710	Primer for reverse
c	39	11.6	64.4	30	17	AAT10031	MDGF cDNA/antisens
c	40	11.6	64.4	30	20	AAX36536	PCR primer for hum
c	41	11.6	64.4	30	21	AAA13756	Stem cell factor u
c	42	11.6	64.4	30	21	AAZ55799	Reverse transcript
c	43	11.6	64.4	30	22	AAS10451	Human stem cell fa
c	44	11.6	64.4	30	22	AAH41335	Universal stem cel
c	45	11.6	64.4	30	22	AAS04115	Human SCF (stem ce

ALIGNMENTS

RESULT 1
AAS12348
ID AAS12348 standard; DNA; 18 BP.
XX
AC AAS12348;
XX
DT 21-NOV-2001 (first entry)
XX
DE DNA encoding deoxyribozyme #8.
XX
KW Deoxyribozyme; cytostatic; endonuclease; RNA cleavage; DNA cleavage;
KW gene therapy; plant; fungus; bacteria; mammal; ribozyme; ss.
XX
OS Synthetic.
XX
PN WO200159102-A2.
XX
PD 16-AUG-2001.
XX
PF 08-FEB-2001; 2001WO-US04223.
XX
PR 08-FEB-2000; 2000US-0181360.
PR 31-MAR-2000; 2000US-0193646.
XX
PA (RIBO-) RIBOZYME PHARM INC.
PA (UYYA) UNIV YALE.
XX
PI Breaker R, Beigelman L, Emilsson G;
XX
DR WPI; 2001-536526/59.
XX
PT New nucleic acids with endonuclease activity, such as ribozymes and

PT nucleozymes, for modulating gene expression in a plant, mammalian,
PT bacterial or fungal cell -
XX
PS Claim 49; Page 77; 96pp; English.
XX
CC The invention relates to nucleic acid molecules with endonuclease
CC activity, which are particularly useful for cleavage of RNA or DNA.
CC The nucleic acids are used in a pharmaceutical composition and are used
CC to modulate expression of a gene in a plant, mammalian, bacterial or
CC fungal cell. They are used to cleave a separate nucleic acid, preferably
CC RNA. The nucleic acids are used to inhibit gene expression and/or cell
CC proliferation, and can be used to treat a disease or condition. More
CC than one nucleic acid can be independently targeted to the same or
CC different sites in a cell. The nucleic acids may be used to study DNA.
CC The modifications to the nucleic acids optimises their catalytic activity
CC and can maintain or enhance their activity. They exhibit a high degree
CC of specificity for RNA. The present sequence represents the coding
CC sequence of deoxyribozyme #8 used in the method of the invention.
XX
SQ Sequence 18 BP; 4 A; 4 C; 6 G; 4 U; 0 other;

Query Match 100.0%; Score 18; DB 22; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.63;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAUGGCCUAUCGGUGCGA 18
||||||||||||||||||
Db 1 AAUGGCCUAUCGGUGCGA 18

RESULT 2
AAS12381
ID AAS12381 standard; RNA; 29 BP.
XX
AC AAS12381;
XX
DT 21-NOV-2001 (first entry)
XX
DE Class IV ribozyme.
XX
KW Deoxyribozyme; cytostatic; endonuclease; RNA cleavage; DNA cleavage;
KW gene therapy; plant; fungus; bacteria; mammal; ribozyme; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT misc_binding 1..8
FT /*tag= a
FT /note= "Forms double-stranded region with bases 15
FT to 8 of AAS12374"
FT misc_binding 25..29
FT /*tag= b
FT /note= "Forms double-stranded region with bases 5
FT to 1 of AAS12374"
XX
PN WO200159102-A2.
XX
PD 16-AUG-2001.
XX
PF 08-FEB-2001; 2001WO-US04223.
XX
PR 08-FEB-2000; 2000US-0181360.
PR 31-MAR-2000; 2000US-0193646.
XX
PA (RIBO-) RIBOZYME PHARM INC.
PA (UYYA) UNIV YALE.
XX
PI Breaker R, Beigelman L, Emilsson G;
XX
DR WPI; 2001-536526/59.
XX
PT New nucleic acids with endonuclease activity, such as ribozymes and
PT nucleozymes, for modulating gene expression in a plant, mammalian,
PT bacterial or fungal cell -
XX
PS Example 1; Fig 9; 96pp; English.
XX
CC The invention relates to nucleic acid molecules with endonuclease
CC activity, which are particularly useful for cleavage of RNA or DNA.
CC The nucleic acids are used in a pharmaceutical composition and are used
CC to modulate expression of a gene in a plant, mammalian, bacterial or
CC fungal cell. They are used to cleave a separate nucleic acid, preferably
CC RNA. The nucleic acids are used to inhibit gene expression and/or cell
CC proliferation, and can be used to treat a disease or condition. More
CC than one nucleic acid can be independently targeted to the same or
CC different sites in a cell. The nucleic acids may be used to study DNA.
CC The modifications to the nucleic acids optimises their catalytic activity
CC and can maintain or enhance their activity. They exhibit a high degree
CC of specificity for RNA. The present sequence represents the Class IV
CC ribozyme, used in an example which demonstrates the method of
CC the invention.
XX
SQ Sequence 29 BP; 6 A; 7 C; 11 G; 5 U; 0 other;

Query Match 100.0%; Score 18; DB 22; Length 29;
Best Local Similarity 100.0%; Pred. No. 0.67;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAUGGCCUAUCGGUGCGA 18
||||||||||||||||||
Db 8 AAUGGCCUAUCGGUGCGA 25

RESULT 3
AAS19241/c
ID AAS19241 standard; DNA; 30 BP.
XX
AC AAS19241;
XX
DT 26-MAR-2002 (first entry)
XX
DE CMV mutagenic adaptor.
XX
KW T0; ds; terminator; pGA; DNA vaccine; anti-HIV; virucide;
KW Human Immunodeficiency Virus; HIV; Gag; HIV gp120; HIV Pol; HIV Env;
KW HIV VLP; measles fusion protein; measles haemagglutinin; CMV; adaptor;
KW measles nucleoprotein; influenza haemagglutinin; C3d gene;
KW cell-mediated immune response; humoral immune response; infection.
XX
OS Human cytomegalovirus.
XX
PN WO200192470-A2.
XX
PD 06-DEC-2001.
XX
PF 02-MAR-2001; 2001WO-US06795.
XX
PR 02-MAR-2000; 2000US-186364P.
PR 01-DEC-2000; 2000US-251083P.
XX
PA (UYEM-) UNIV EMORY.
XX
PI Robinson HL, Smith JM, Ross TM, Bright RA, Hua J, Ellenberger D;
XX
DR WPI; 2002-075465/10.
XX
PT Novel pGA vector useful for immunising patient against measles,
PT influenza has termination sequence encoding lambda T0 terminator and a
PT eukaryotic transcription cassette with vaccine insert encoding
PT immunogens of pathogens -
XX
PS Example 2; Page 43; 174pp; English.
XX
CC The invention relates to a vector (a pGA construct) comprising a
CC termination sequence coding for the lambda T0 terminator, a prokaryotic
CC origin of replication, a selectable marker gene and a eukaryotic

CC transcription cassette comprising a vaccine insert encoding one or more
CC immunogens derived from a pathogen e.g. Human Immunodeficiency Virus
CC (HIV) Gag, HIV gp120, HIV Pol, HIV Env, HIV VLP, or its mutants, measles
CC fusion protein, measles haemagglutinin, measles nucleoprotein, influenza
CC haemagglutinin, or its mutants, or subsequences, and optionally at least
CC one C3d gene, is useful for immunising or treating a patient, when
CC administered by an intramuscular or intradermal route. The immunisation
CC methods using pGA elicit both cell-mediated and humoral immune responses
CC that may limit the infection, spread or growth of the pathogen and result
CC in protection against subsequent challenge against the pathogen. The
CC terminator sequence present prevents read-through from the kanamycin
CC cassette into vaccine sequences while the plasmid is being produced in
CC bacteria. Prevention of transcriptional read-through stabilises vaccine
CC insert sequences by limiting the exposure of secondary structures that
CC can be recognised by bacterial endonucleases. The present sequence
CC is an adaptor for introducing a ClaI site into the cytomegalovirus
CC (CMV) promoter of pGA2.
XX
SQ Sequence 30 BP; 7 A; 12 C; 6 G; 5 T; 0 other;

Query Match 76.7%; Score 13.8; DB 24; Length 30;
Best Local Similarity 64.7%; Pred. No. 1.9e+02;
Matches 11; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 2 AUGGCCUAUCGGUGCGA 18
|:||| :|:|| :||||
Db 25 ATGGCGTATCGATGCGA 9

RESULT 4
ABN47743
ID ABN47743 standard; DNA; 60 BP.
XX
AC ABN47743;
XX
DT 15-JUL-2002 (first entry)
XX
DE Human spliced transcript detection oligonucleotide SEQ ID NO:20491.
XX
KW Human; mouse; rat; splice transcript; detection; RNA transcript;
KW splice variant; transcriptome; oligonucleotide library; ss.
XX
OS Homo sapiens.
XX
PN WO200210449-A2.
XX
PD 07-FEB-2002.
XX
PF 20-JUL-2001; 2001WO-IB01903.
XX
PR 28-JUL-2000; 2000US-221607P.
PR 02-MAY-2001; 2001US-287724P.
XX
PA (COMP-) COMPUGEN INC.
XX
PI Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;
XX
DR WPI; 2002-257383/30.
XX
PT New oligonucleotide libraries comprising oligonucleotides which
PT selectively hybridize to mRNAs transcribed from a transcription unit of
PT a genome, useful for detecting tissue-, pathology-, and
PT developmental-specific genes -
XX
PS Example 1; SEQ ID 20491; 47pp; English.
XX
CC The present invention describes oligonucleotide libraries for detecting
CC messenger RNAs that populate a (sub-)transcriptome, where the
CC (sub-)transcriptome comprises messenger RNAs transcribed from multiple
CC transcription units that populate a genome. The library comprises
CC several oligonucleotides, each capable of hybridising selectively to a
CC set of messenger RNAs transcribed from a given transcription unit of
CC the genome, which encodes one or more messenger RNA splice variants.
CC The oligonucleotide libraries are useful for detecting mRNAs from a
CC biological sample, in expression profiling studies, in qualitatively or
CC quantitatively characterising the corresponding transcriptome, and in
CC detecting RNA transcripts and splice variants of human or animal
CC transcriptomes. The libraries may also be used as specialised mini
CC libraries to detect transcripts of a sub-transcriptome under a
CC particular biological or pathological state, and so allowing the
CC detection of tissue- and pathology-specific genes such as those genes
CC only expressed in specific tissue under a specific pathological
CC condition; to detect developmental specific genes; and to detect RNA
CC transcripts and splice variants of a transcriptome of a patient suffering
CC from a particular disorder. ABN27253 to ABN59589 represent
CC oligonucleotide sequences from rats, humans and mice, which are used in
CC the exemplification of the present invention.
CC N.B. The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 60 BP; 16 A; 18 C; 13 G; 13 T; 0 other;

Query Match 74.4%; Score 13.4; DB 24; Length 60;
Best Local Similarity 66.7%; Pred. No. 3.6e+02;
Matches 10; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AAUGGCCUAUCGGUG 15
| :|||||:|:|||:|
Db 1 ATTGGCCTATCGGTG 15

RESULT 5
ABI95945
ID ABI95945 standard; DNA; 20 BP.
XX
AC ABI95945;
XX
DT 16-FEB-2002 (first entry)
XX
DE Capture oligonucleptide Zip ID#3032 oligo #9.
XX
KW Human; K-ras; PCR primer; probe; capture probe; mutation detection;
KW ligase detection reaction; LDR; p53; BRCA1; BRCA2; infectious disease;
KW infection; 21 hydroxylase deficiency; Turner Syndrome; obesity;
KW cancer; oncogene; tumour suppressor; human papillomavirus; forensic;
KW environmental monitoring; food industry; feed industry; ss.
XX
OS Synthetic.
XX
PN WO200179548-A2.
XX
PD 25-OCT-2001.
XX
PF 04-APR-2001; 2001WO-US10958.
XX
PR 14-APR-2000; 2000US-197271P.
XX
PA (CORR) CORNELL RES FOUND INC.
XX
PI Barany F, Zirvi M, Gerry NP, Favis R, Kliman R;
XX
DR WPI; 2002-034366/04.
XX
PT Designing capture oligonucleotide probes for use on a support to which
PT complementary oligonucleotides hybridize with little mismatch -
XX
PS Example 5; Fig 29; 300pp; English.
XX
CC The present invention describes a method (M1) for designing capture
CC oligonucleotide probes (I) for use on a support to which complementary
CC oligonucleotide probes (II) will hybridise with little mismatch, where
CC (I) have melting temperatures within a narrow range. The method is useful
CC for detecting infectious diseases caused by bacterial infectious agents
CC e.g. Salmonella, Listeria monocytogenes and Haemophilus influenza, fungal
CC infectious agents e.g. Cryptococcus neoformans, Candida albicans and

CC Aspergillus fumigautus, viruses e.g. T-cell lymphocytotrophis cirus,
CC Epstein-Barr virus and polio virus, and parasitic infectious agents
CC selected from Onchoverva volvulus, Entamoeba histolytica and Dracunculus
CC medinesis. The method is also useful for detecting genetic diseases such
CC as 21 hydroxylase deficiency, Turner Syndrome and obesity defects.
CC Detecting cancer involving oncogenes, tumour suppressor genes, or genes
CC involved in DNA amplification, replication, recombination or repair, the
CC cancer is specifically associated with a gene selected from BRCA1 gene,
CC p53 gene, human papillomavirus types 16 and 18 and liver cancers. The
CC method is also used for environmental monitoring, forensics and the food
CC and feed industry, detecting comprises scanning (using e.g. a scanning
CC electron microscope and infrared microscope) the support at the
CC particular sites and identifying if ligation of the oligonucleotide probe
CC sets occurred and correlating (using a computer) identified ligation to a
CC presence or absence of the target nucleotide sequences. ABI82074 to
CC ABI97546 represent oligonucleotide sequences used in the exemplification
CC of the present invention.
XX
SQ Sequence 20 BP; 2 A; 6 C; 6 G; 6 T; 0 other;

Query Match 71.1%; Score 12.8; DB 24; Length 20;
Best Local Similarity 68.8%; Pred. No. 7.2e+02;
Matches 11; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 2 AUGGCCUAUCGGUGCG 17
| ||| :|:|||:|||
Db 2 ACGGCTTATCGGTGCG 17

RESULT 6
ABI88460
ID ABI88460 standard; DNA; 24 BP.
XX
AC ABI88460;
XX
DT 15-FEB-2002 (first entry)
XX
DE Capture oligonucleotide Zip ID#3032 oligo #1.
XX
KW Human; K-ras; PCR primer; probe; capture probe; mutation detection;
KW ligase detection reaction; LDR; p53; BRCA1; BRCA2; infectious disease;
KW infection; 21 hydroxylase deficiency; Turner Syndrome; obesity;
KW cancer; oncogene; tumour suppressor; human papillomavirus; forensic;
KW environmental monitoring; food industry; feed industry; ss.
XX
OS Synthetic.
XX
PN WO200179548-A2.
XX
PD 25-OCT-2001.
XX
PF 04-APR-2001; 2001WO-US10958.
XX
PR 14-APR-2000; 2000US-197271P.
XX
PA (CORR) CORNELL RES FOUND INC.
XX
PI Barany F, Zirvi M, Gerry NP, Favis R, Kliman R;
XX
DR WPI; 2002-034366/04.
XX
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PT complementary oligonucleotides hybridize with little mismatch -
XX
PS Example 5; Fig 25; 300pp; English.
XX
CC The present invention describes a method (M1) for designing capture
CC oligonucleotide probes (I) for use on a support to which complementary
CC oligonucleotide probes (II) will hybridise with little mismatch, where
CC (I) have melting temperatures within a narrow range. The method is useful
CC for detecting infectious diseases caused by bacterial infectious agents
CC e.g. Salmonella, Listeria monocytogenes and Haemophilus influenza, fungal
CC infectious agents e.g. Cryptococcus neoformans, Candida albicans and

CC Aspergillus fumigautus, viruses e.g. T-cell lymphocytotrophis cirus,
CC Epstein-Barr virus and polio virus, and parasitic infectious agents
CC selected from Onchoverva volvulus, Entamoeba histolytica and Dracunculus
CC medinesis. The method is also useful for detecting genetic diseases such
CC as 21 hydroxylase deficiency, Turner Syndrome and obesity defects.
CC Detecting cancer involving oncogenes, tumour suppressor genes, or genes
CC involved in DNA amplification, replication, recombination or repair, the
CC cancer is specifically associated with a gene selected from BRCA1 gene,
CC p53 gene, human papillomavirus types 16 and 18 and liver cancers. The
CC method is also used for environmental monitoring, forensics and the food
CC and feed industry, detecting comprises scanning (using e.g. a scanning
CC electron microscope and infrared microscope) the support at the
CC particular sites and identifying if ligation of the oligonucleotide probe
CC sets occurred and correlating (using a computer) identified ligation to a
CC presence or absence of the target nucleotide sequences. ABI82074 to
CC ABI97546 represent oligonucleotide sequences used in the exemplification
CC of the present invention.
XX
SQ Sequence 24 BP; 2 A; 7 C; 7 G; 8 T; 0 other;

Query Match 71.1%; Score 12.8; DB 24; Length 24;
Best Local Similarity 68.8%; Pred. No. 7.3e+02;
Matches 11; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 2 AUGGCCUAUCGGUGCG 17
| ||| :|:|||:|||
Db 2 ACGGCTTATCGGTGCG 17

RESULT 7
ABI88461/c
ID ABI88461 standard; DNA; 24 BP.
XX
AC ABI88461;
XX
DT 15-FEB-2002 (first entry)
XX
DE Capture oligonucleotide Zip ID#3032 oligo #2.
XX
KW Human; K-ras; PCR primer; probe; capture probe; mutation detection;
KW ligase detection reaction; LDR; p53; BRCA1; BRCA2; infectious disease;
KW infection; 21 hydroxylase deficiency; Turner Syndrome; obesity;
KW cancer; oncogene; tumour suppressor; human papillomavirus; forensic;
KW environmental monitoring; food industry; feed industry; ss.
XX
OS Synthetic.
XX
PN WO200179548-A2.
XX
PD 25-OCT-2001.
XX
PF 04-APR-2001; 2001WO-US10958.
XX
PR 14-APR-2000; 2000US-197271P.
XX
PA (CORR) CORNELL RES FOUND INC.
XX
PI Barany F, Zirvi M, Gerry NP, Favis R, Kliman R;
XX
DR WPI; 2002-034366/04.
XX
PT Designing capture oligonucleotide probes for use on a support to which
PT complementary oligonucleotides hybridize with little mismatch -
XX
PS Example 5; Fig 25; 300pp; English.
XX
CC The present invention describes a method (M1) for designing capture
CC oligonucleotide probes (I) for use on a support to which complementary
CC oligonucleotide probes (II) will hybridise with little mismatch, where
CC (I) have melting temperatures within a narrow range. The method is useful
CC for detecting infectious diseases caused by bacterial infectious agents
CC e.g. Salmonella, Listeria monocytogenes and Haemophilus influenza, fungal
CC infectious agents e.g. Cryptococcus neoformans, Candida albicans and

CC Aspergillus fumigautus, viruses e.g. T-cell lymphocytotrophis cirus,
CC Epstein-Barr virus and polio virus, and parasitic infectious agents
CC selected from Onchoverva volvulus, Entamoeba histolytica and Dracunculus
CC medinesis. The method is also useful for detecting genetic diseases such
CC as 21 hydroxylase deficiency, Turner Syndrome and obesity defects.
CC Detecting cancer involving oncogenes, tumour suppressor genes, or genes
CC involved in DNA amplification, replication, recombination or repair, the
CC cancer is specifically associated with a gene selected from BRCA1 gene,
CC p53 gene, human papillomavirus types 16 and 18 and liver cancers. The
CC method is also used for environmental monitoring, forensics and the food
CC and feed industry, detecting comprises scanning (using e.g. a scanning
CC electron microscope and infrared microscope) the support at the
CC particular sites and identifying if ligation of the oligonucleotide probe
CC sets occurred and correlating (using a computer) identified ligation to a
CC presence or absence of the target nucleotide sequences. ABI82074 to
CC ABI97546 represent oligonucleotide sequences used in the exemplification
CC of the present invention.
XX
SQ Sequence 24 BP; 8 A; 7 C; 7 G; 2 T; 0 other;

Query Match 71.1%; Score 12.8; DB 24; Length 24;
Best Local Similarity 68.8%; Pred. No. 7.3e+02;
Matches 11; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 2 AUGGCCUAUCGGUGCG 17
| ||| :|:|||:|||
Db 23 ACGGCTTATCGGTGCG 8

RESULT 8
AAC87378
ID AAC87378 standard; DNA; 41 BP.
XX
AC AAC87378;
XX
DT 09-MAR-2001 (first entry)
XX
DE Staphylococcus aureus SpA domain D antisense PCR primer, PC3H AS.
XX
KW SpA domain D; randomised library; VH3 Ig-Fab fragment; immunoglobulin;
KW SpA mutant; superantigen; altered specificity; apoptosis inducer;
KW anergy inducer; B-lymphocyte subset; B-cell; lymphoma; leukaemia;
KW autoimmune disease; idiopathic thrombocytopenia; rheumatoid arthritis;
KW systemic lupus erythematosus; SLE; autoimmune thyroiditis; diabetes.
KW antibody purification; PCR primer; ss.
XX
OS Staphylococcus aureus.
XX
PN WO200069457-A1.
XX
PD 23-NOV-2000.
XX
PF 15-MAY-2000; 2000WO-US13402.
XX
PR 15-MAY-1999; 99US-0134386.
XX
PA (UYCA-) UNIV CALIFORNIA SAN DIEGO.
XX
PI Silverman GJ;
XX
DR WPI; 2001-031886/04.
XX
PT New staphylococcal protein A variant, useful for treating diabetes and
PT rheumatoid arthritis, exhibits binding specificity for
PT immunoglobulin-Fab domain and comprises variations in amino acid
PT sequence of staphylococcal protein A domain D -
XX
PS Example 12; Page 58; 88pp; English.
XX
CC The invention relates to staphylococcal protein A (SpA) variants which
CC exhibit altered binding specificity for an immunoglobulin Fab (Ig-FAb)
CC fragment relative to native SpA. The SpA variants of the invention have
CC one or more amino acid substitution in the SpA VH3 Ig-Fab binding region
CC (i.e., SpA domain D) relative to the native SpA. The SpA variants are
CC inducers of autoreactive B cell, leukaemic or lymphoma cell apoptosis or
CC anergy. The SpA variants of the invention are useful for detecting the
CC presence of a certain Ig-Fab-expressing lymphocyte subset in a sample of
CC lymphocytes. The SpA variants may therefore be used in the diagnosis of
CC some forms of leukaemia. The SpA variants may also be administered to an
CC individual with an abnormally high number of a certain lymphocyte subset
CC to reduce the number of that lymphocyte subset. The SpA variants are
CC also useful for purifying monoclonal or polyclonal antibodies from
CC serum, plasma, tissue culture or other sources. The SpA variants that
CC exhibit enhanced clan VH3-specific effects in vitro or in vivo, such as
CC the ability to delete undesirable neoplastic B-cells or pathogenic
CC B-cells that are responsible for the production of disease-causing
CC autoantibodies, are useful as therapeutic agents. Therapeutic SpA
CC variants that can bind to Fab on the B-cell receptor of an autoreactive
CC B-cell or leukaemic or lymphoma cell can induce anergy, apoptosis, or
CC deletion by other mechanisms. By engineering the interaction between SpA
CC variants and Ig-Fab according to the invention, variant SpA with
CC specially tailored Fab-binding specificities can be selected that target
CC pathogenic neoplastic B cell populations or autoreactive B-cell
CC clones. The SpA variants are therefore useful for treating conditions
CC that are linked to disease-associated B-cells such as idiopathic
CC thrombocytopenia, rheumatoid arthritis, systemic lupus erythematosus
CC (SLE), autoimmune thyroiditis, or diabetes. Engineered B cell
CC superantigens (such as the SpA variants of the invention) bind to
CC immunoglobulin receptors on B-cells in a manner that is distinct from
CC antigen binding by antibodies. Therefore, the SpA variants which
CC have superantigen properties can target much larger populations of
CC Ig-expressing B cells in vivo compared with targetting using a specific
CC antigen. Sequences AAC87372-C87378 represent nucleic acid sequences
CC used in the construction of a randomised SpA domain D library in
CC an exemplification of the invention. Sequences AAC87375-C87378 represent
CC SpA domain D PCR primers used in library construction.
XX
SQ Sequence 41 BP; 5 A; 9 C; 19 G; 8 T; 0 other;

Query Match 68.9%; Score 12.4; DB 22; Length 41;
Best Local Similarity 64.3%; Pred. No. 1.3e+03;
Matches 9; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 3 UGGCCUAUCGGUGC 16
:|||| : :|||:||
Db 23 TGGCCTTTCGGTGC 36

RESULT 9
ABI93941
ID ABI93941 standard; DNA; 20 BP.
XX
AC ABI93941;
XX
DT 16-FEB-2002 (first entry)
XX
DE Capture oligonucleptide Zip ID#1028 oligo #9.
XX
KW Human; K-ras; PCR primer; probe; capture probe; mutation detection;
KW ligase detection reaction; LDR; p53; BRCA1; BRCA2; infectious disease;
KW infection; 21 hydroxylase deficiency; Turner Syndrome; obesity;
KW cancer; oncogene; tumour suppressor; human papillomavirus; forensic;
KW environmental monitoring; food industry; feed industry; ss.
XX
OS Synthetic.
XX
PN WO200179548-A2.
XX
PD 25-OCT-2001.
XX
PF 04-APR-2001; 2001WO-US10958.
XX
PR 14-APR-2000; 2000US-197271P.
XX
PA (CORR) CORNELL RES FOUND INC.
XX

PI Barany F, Zirvi M, Gerry NP, Favis R, Kliman R;
XX
DR WPI; 2002-034366/04.
XX
PT Designing capture oligonucleotide probes for use on a support to which
PT complementary oligonucleotides hybridize with little mismatch -
XX
PS Example 5; Fig 29; 300pp; English.
XX
CC The present invention describes a method (M1) for designing capture
CC oligonucleotide probes (I) for use on a support to which complementary
CC oligonucleotide probes (II) will hybridise with little mismatch, where
CC (I) have melting temperatures within a narrow range. The method is useful
CC for detecting infectious diseases caused by bacterial infectious agents
CC e.g. Salmonella, Listeria monocytogenes and Haemophilus influenza, fungal
CC infectious agents e.g. Cryptococcus neoformans, Candida albicans and
CC Aspergillus fumigautus, viruses e.g. T-cell lymphocytotrophis cirus,
CC Epstein-Barr virus and polio virus, and parasitic infectious agents
CC selected from Onchoverva volvulus, Entamoeba histolytica and Dracunculus
CC medinesis. The method is also useful for detecting genetic diseases such
CC as 21 hydroxylase deficiency, Turner Syndrome and obesity defects.
CC Detecting cancer involving oncogenes, tumour suppressor genes, or genes
CC involved in DNA amplification, replication, recombination or repair, the
CC cancer is specifically associated with a gene selected from BRCA1 gene,
CC p53 gene, human papillomavirus types 16 and 18 and liver cancers. The
CC method is also used for environmental monitoring, forensics and the food
CC and feed industry, detecting comprises scanning (using e.g. a scanning
CC electron microscope and infrared microscope) the support at the
CC particular sites and identifying if ligation of the oligonucleotide probe
CC sets occurred and correlating (using a computer) identified ligation to a
CC presence or absence of the target nucleotide sequences. ABI82074 to
CC ABI97546 represent oligonucleotide sequences used in the exemplification
CC of the present invention.
XX
SQ Sequence 20 BP; 7 A; 6 C; 4 G; 3 T; 0 other;

Query Match 67.8%; Score 12.2; DB 24; Length 20;
Best Local Similarity 64.7%; Pred. No. 1.6e+03;
Matches 11; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 2 AUGGCCUAUCGGUGCGA 18
|:| || |:|| :||||
Db 3 ATGACCAATCGATGCGA 19

RESULT 10
AAS08711/c
ID AAS08711 standard; DNA; 24 BP.
XX
AC AAS08711;
XX
DT 26-SEP-2001 (first entry)
XX
DE Human PD-ATP-binding cassette (PD-ABC) cDNA reverse PCR primer #2.
XX
KW PD-ATP-binding cassette; PD-ABC; chromosome 19p13.3; spleen; thymus; ss;
KW peripheral blood leukocyte; bone marrow; lymph node; dyslipidaemia;
KW cardiovascular disorder; inflammatory disorder; abnormal calcium flux;
KW epilepsy; coronary artery disease; Tangier's disease; atherosclerosis;
KW familial high-density lipoprotein deficiency; fatty liver disease;
KW atherosclerosis; diabetes; insulin resistance; obesity; drug screening;
KW alcoholism; retinal degeneration; hypertension; vascular disease;
KW PCR primer.
XX
OS Synthetic.
XX
PN WO200153490-A1.
XX
PD 26-JUL-2001.
XX
PF 23-JAN-2001; 2001WO-US02191.
XX
PR 24-JAN-2000; 2000US-0177889.
XX
PR 30-JUN-2000; 2000US-0215405.
XX
PA (WARN) WARNER LAMBERT CO.
XX
PI Johns MA, Tafuri SR, Wang M;
XX
DR WPI; 2001-442259/47.
XX
PT New Human PD-ABC DNA molecules and proteins for diagnosis and treatment
PT of dyslipidaemia, epilepsy and diseases related to abnormal calcium flux
PT -
XX
PS Disclosure; Page 34; 77pp; English.
XX
CC The sequence represents a PCR primer used for isolation of cDNA encoding
CC human PD-ATP-binding cassette (PD-ABC) protein. PD-ABC maps to chromosome
CC 19p13.3 and is expressed in various tissues including spleen, thymus,
CC peripheral blood leukocytes, bone marrow and lymph nodes. The PD-ABC DNA
CC molecules and proteins are used to diagnose and treat cardiovascular
CC disorders, inflammatory disorders, dyslipidaemia, epilepsy, diseases
CC related to abnormal calcium flux, coronary artery disease, Tangier's
CC disease, familial high-density lipoprotein deficiency, atherosclerosis,
CC diabetes, fatty liver disease, insulin resistance, obesity, alcoholism,
CC retinal degeneration, hypertension and vascular disease. The sequences
CC are also used in drug screening assays.
XX
SQ Sequence 24 BP; 7 A; 6 C; 7 G; 4 T; 0 other;

Query Match 67.8%; Score 12.2; DB 22; Length 24;
Best Local Similarity 58.8%; Pred. No. 1.6e+03;
Matches 10; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 2 AUGGCCUAUCGGUGCGA 18
|:| ||:|:| |:|| |
Db 24 ATGCCCTATCCGTGCTA 8

RESULT 11
ABI84452
ID ABI84452 standard; DNA; 24 BP.
XX
AC ABI84452;
XX
DT 15-FEB-2002 (first entry)
XX
DE Capture oligonucleotide Zip ID#1028 oligo #1.
XX
KW Human; K-ras; PCR primer; probe; capture probe; mutation detection;
KW ligase detection reaction; LDR; p53; BRCA1; BRCA2; infectious disease;
KW infection; 21 hydroxylase deficiency; Turner Syndrome; obesity;
KW cancer; oncogene; tumour suppressor; human papillomavirus; forensic;
KW environmental monitoring; food industry; feed industry; ss.
XX
OS Synthetic.
XX
PN WO200179548-A2.
XX
PD 25-OCT-2001.
XX
PF 04-APR-2001; 2001WO-US10958.
XX
PR 14-APR-2000; 2000US-197271P.
XX
PA (CORR) CORNELL RES FOUND INC.
XX
PI Barany F, Zirvi M, Gerry NP, Favis R, Kliman R;
XX
DR WPI; 2002-034366/04.
XX
PT Designing capture oligonucleotide probes for use on a support to which
PT complementary oligonucleotides hybridize with little mismatch -
XX
PS Example 5; Fig 25; 300pp; English.

XX
CC The present invention describes a method (M1) for designing capture
CC oligonucleotide probes (I) for use on a support to which complementary
CC oligonucleotide probes (II) will hybridise with little mismatch, where
CC (I) have melting temperatures within a narrow range. The method is useful
CC for detecting infectious diseases caused by bacterial infectious agents
CC e.g. Salmonella, Listeria monocytogenes and Haemophilus influenza, fungal
CC infectious agents e.g. Cryptococcus neoformans, Candida albicans and
CC Aspergillus fumigautus, viruses e.g. T-cell lymphocytotrophis cirus,
CC Epstein-Barr virus and polio virus, and parasitic infectious agents
CC selected from Onchoverva volvulus, Entamoeba histolytica and Dracunculus
CC medinesis. The method is also useful for detecting genetic diseases such
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CC involved in DNA amplification, replication, recombination or repair, the
CC cancer is specifically associated with a gene selected from BRCA1 gene,
CC p53 gene, human papillomavirus types 16 and 18 and liver cancers. The
CC method is also used for environmental monitoring, forensics and the food
CC and feed industry, detecting comprises scanning (using e.g. a scanning
CC electron microscope and infrared microscope) the support at the
CC particular sites and identifying if ligation of the oligonucleotide probe
CC sets occurred and correlating (using a computer) identified ligation to a
CC presence or absence of the target nucleotide sequences. ABI82074 to
CC ABI97546 represent oligonucleotide sequences used in the exemplification
CC of the present invention.
XX
SQ Sequence 24 BP; 7 A; 7 C; 5 G; 5 T; 0 other;

Query Match 67.8%; Score 12.2; DB 24; Length 24;
Best Local Similarity 64.7%; Pred. No. 1.6e+03;
Matches 11; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 2 AUGGCCUAUCGGUGCGA 18
|:| || |:|| :||||
Db 7 ATGACCAATCGATGCGA 23

RESULT 12
ABI84453/c
ID ABI84453 standard; DNA; 24 BP.
XX
AC ABI84453;
XX
DT 15-FEB-2002 (first entry)
XX
DE Capture oligonucleotide Zip ID#1028 oligo #2.
XX
KW Human; K-ras; PCR primer; probe; capture probe; mutation detection;
KW ligase detection reaction; LDR; p53; BRCA1; BRCA2; infectious disease;
KW infection; 21 hydroxylase deficiency; Turner Syndrome; obesity;
KW cancer; oncogene; tumour suppressor; human papillomavirus; forensic;
KW environmental monitoring; food industry; feed industry; ss.
XX
OS Synthetic.
XX
PN WO200179548-A2.
XX
PD 25-OCT-2001.
XX
PF 04-APR-2001; 2001WO-US10958.
XX
PR 14-APR-2000; 2000US-197271P.
XX
PA (CORR) CORNELL RES FOUND INC.
XX
PI Barany F, Zirvi M, Gerry NP, Favis R, Kliman R;
XX
DR WPI; 2002-034366/04.
XX
PT Designing capture oligonucleotide probes for use on a support to which
PT complementary oligonucleotides hybridize with little mismatch -
XX
PS Example 5; Fig 25; 300pp; English.

XX
CC The present invention describes a method (M1) for designing capture
CC oligonucleotide probes (I) for use on a support to which complementary
CC oligonucleotide probes (II) will hybridise with little mismatch, where
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CC e.g. Salmonella, Listeria monocytogenes and Haemophilus influenza, fungal
CC infectious agents e.g. Cryptococcus neoformans, Candida albicans and
CC Aspergillus fumigautus, viruses e.g. T-cell lymphocytotrophis cirus,
CC Epstein-Barr virus and polio virus, and parasitic infectious agents
CC selected from Onchoverva volvulus, Entamoeba histolytica and Dracunculus
CC medinesis. The method is also useful for detecting genetic diseases such
CC as 21 hydroxylase deficiency, Turner Syndrome and obesity defects.
CC Detecting cancer involving oncogenes, tumour suppressor genes, or genes
CC involved in DNA amplification, replication, recombination or repair, the
CC cancer is specifically associated with a gene selected from BRCA1 gene,
CC p53 gene, human papillomavirus types 16 and 18 and liver cancers. The
CC method is also used for environmental monitoring, forensics and the food
CC and feed industry, detecting comprises scanning (using e.g. a scanning
CC electron microscope and infrared microscope) the support at the
CC particular sites and identifying if ligation of the oligonucleotide probe
CC sets occurred and correlating (using a computer) identified ligation to a
CC presence or absence of the target nucleotide sequences. ABI82074 to
CC ABI97546 represent oligonucleotide sequences used in the exemplification
CC of the present invention.
XX
SQ Sequence 24 BP; 5 A; 5 C; 7 G; 7 T; 0 other;

Query Match 67.8%; Score 12.2; DB 24; Length 24;
Best Local Similarity 64.7%; Pred. No. 1.6e+03;
Matches 11; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 2 AUGGCCUAUCGGUGCGA 18
|:| || |:|| :||||
Db 18 ATGACCAATCGATGCGA 2

RESULT 13
AAX98255/c
ID AAX98255 standard; DNA; 29 BP.
XX
AC AAX98255;
XX
DT 25-OCT-1999 (first entry)
XX
DE PCR primer used to amplify a 1659 bp fragment containing ORF1.
XX
KW Human pathogen; virulence polypeptide; virulence factor;
KW pathogenic infection; Pseudomonas aeruginosa infection; PCR primer; ss.
XX
OS Synthetic.
OS Pseudomonas aeruginosa.
XX
PN WO9927129-A1.
XX
PD 03-JUN-1999.
XX
PF 25-NOV-1998; 98WO-US25247.
XX
PR 25-NOV-1997; 97US-0066517.
XX
PA (GEHO) GEN HOSPITAL CORP.
XX
PI Ausubel F, Cao H, Drenkard E, Goodman HM, Mahajan-Miklos S;
PI Rahme LG, Tan M, Tsongalis J;
XX
DR WPI; 1999-357851/30.
XX
PT Virulence factors useful in developing disease treatments
XX
PS Disclosure; Page 26; 228pp; English.
XX
CC The present sequence represents a PCR primer used to amplify Pseudomonas

CC aeruginosa nucleic acid sequences, in the course of the invention.
CC P. aeruginosa is an opportunistic human pathogen present in soil
CC water and plants. The specification describes virulence polypeptides
CC and nucleic acid sequence encoding such polypeptides. These sequences
CC can be used to identify a compound which is capable of decreasing the
CC expression of a pathogenic virulence factor. Compounds that inhibit
CC the expression or activity of virulence factor polypeptides can be
CC used to treat pathogenic infections, especially where the infection
CC is a P. aeruginosa infection.
XX
SQ Sequence 29 BP; 6 A; 10 C; 8 G; 5 T; 0 other;

Query Match 67.8%; Score 12.2; DB 20; Length 29;
Best Local Similarity 64.7%; Pred. No. 1.7e+03;
Matches 11; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 AAUGGCCUAUCGGUGCG 17
|| ||| :|:|| :|||
Db 19 AACGGCGTATCGTTGCG 3

RESULT 14
AAT70787/c
ID AAT70787 standard; RNA; 40 BP.
XX
AC AAT70787;
XX
DT 30-JUL-1997 (first entry)
XX
DE Stenotic carotid artery binding ligand Civ19.
XX
KW Ligand; peripheral blood mononuclear cell; fibrin clot; carotid artery;
KW systematic evolution of ligands by exponential enrichment method; PBMC;
KW epitope; macromolecule; tissue SELEX method; cancer screening; therapy;
KW AIDS monitoring; localisation of thrombi; atherosclerosis; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1..40
FT /*tag= a
FT /mod_base= all C's are 2-fluorine-C
FT modified_base 1..40
FT /*tag= b
FT /mod_base= all U's are 2-fluorine-U
XX
PN WO9634874-A1.
XX
PD 07-NOV-1996.
XX
PF 01-MAY-1996; 96WO-US06059.
XX
PR 03-MAY-1995; 95US-0433126.
PR 03-MAY-1995; 95US-0433124.
XX
PA (NEXS-) NEXSTAR PHARM INC.
PA (SCHD) SCHERING AG.
XX
PI Gold L, Schneider DJ, Speck U, Stephens A;
XX
DR WPI; 1996-506091/50.
XX
PT Nucleic acid ligands used in cancer screening, AIDS monitoring etc.
PT - bind to peripheral blood mononuclear cells, fibrin clots or
PT carotid arteries
XX
PS Claim 23; Page 58; 138pp; English.
XX
CC AAT70705-T70803 represent the random regions from a degenerate ssDNA
CC library based on the sequence represented by AAT42819. These sequences
CC are all ligands specific for fibrin clots identified using the method of
CC the invention. The method of the invention is for identifying nucleic
CC acid (NA) ligands and NA ligand sequences to a tissue target selected
CC from peripheral blood mononuclear cells (PBMC's) (such as the ligands
CC represented by AAT70584-T70616), fibrin clots (such as the ligands
CC represented by AAT70617-T70704), and carotid arteries (such as these
CC ligands). The method comprises preparing a candidate mixture of NA
CC sequences, and contacting these with the tissue, whereby NAs having an
CC increased affinity to the tissue relative to the candidate mixture may
CC be partitioned from the remainder of the candidate mixture. The
CC increased affinity NAs are then partitioned from the remainder of the
CC candidate mixture, and are amplified to yield a mixture of NAs enriched
CC for NA sequences with a relatively higher affinity and specificity for
CC binding to the tissue, whereby NA ligands of the tissue may be
CC identified. The method represents a tissue SELEX (systematic evolution of
CC ligands by exponential enrichment) method. The NA ligands and epitopes
CC and macromolecules identified using the ligands can be used in diagnostic
CC and therapeutic applications. In particular, they can be used for e.g.
CC cancer screening, AIDS monitoring, detection and localisation of thrombi
CC or atherosclerosis diagnosis and therapy.
XX
SQ Sequence 40 BP; 9 A; 13 C; 8 G; 10 U; 0 other;

Query Match 67.8%; Score 12.2; DB 17; Length 40;
Best Local Similarity 64.7%; Pred. No. 1.8e+03;
Matches 11; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 2 AUGGCCUAUCGGUGCGA 18
| |||| : :||| : |||
Db 21 AAGGCCTTTCGGTCCGA 5

RESULT 15
AAT21824/c
ID AAT21824 standard; cDNA to mRNA; 53 BP.
XX
AC AAT21824;
XX
DT 01-AUG-1996 (first entry)
XX
DE Human gene signature HUMGS03315.
XX
KW Gene signature; messenger RNA; mRNA; relative abundance; frequency;
KW human; cloning; mapping; non-biased library; diagnosis; detection;
KW cell typing; abnormal cell function; ss.
XX
OS Homo sapiens.
XX
PN WO9514772-A1.
XX
PD 01-JUN-1995.
XX
PF 11-NOV-1994; 94WO-JP01916.
XX
PR 12-NOV-1993; 93JP-0355504.
XX
PA (MATS/) MATSUBARA K.
PA (OKUB/) OKUBO K.
XX
PI Matsubara K, Okubo K;
XX
DR WPI; 1995-206931/27.
XX
PT Identifying gene signatures in 3'-directed human cDNA library - e.g.
PT for diagnosis of abnormal cell function, by preparing cDNA that
PT reflects relative abundance of corresp. mRNA in specific human
PT tissues
XX
PS Claim 1; Page 975; 2245pp; Japanese.
XX
CC A single-stranded DNA (or its complementary strand or the corresp.
CC double-stranded DNA) which comprises one of the 7837 "GS" sequences
CC given in AAT19001-T26837 and which is able to hybridise to part of
CC human genomic DNA, cDNA or mRNA is claimed. The GS (Gene Signature)
CC sequences were obtained from 3'-directed cDNA libraries prepared
CC from various human tissues; synthesis of cDNA was initiated from the

```
CC   3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-
CC   untranslated sequence is unique to a particular mRNA species, almost
CC   all the 3'-oriented cDNAs hybridise with specific mRNAs. Each library
CC   is constructed so as to reflect accurately the relative abundance of
CC   different mRNAs in the particular tissue from which it was derived.
CC   The appearance frequency of a given GS in a cDNA library can be
CC   determined (esp. using primers and probes derived from the GS
CC   sequences) as a means of diagnosing abnormal cell function or for
CC   recognising different cell types.
XX
SQ   Sequence 53 BP; 14 A; 11 C; 12 G; 15 T; 1 other;

  Query Match             67.8%;  Score 12.2;  DB 16;  Length 53;
  Best Local Similarity   64.7%;  Pred. No. 1.8e+03;
  Matches   11;  Conservative    3;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 AAUGGCCUAUCGGUGCG 17
              ||:||||  :|| :|||
Db         34 AATGGCCCCTCGATGCG 18


Search completed: July  6, 2003, 14:32:53
Job time : 194.091 secs
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: July 6, 2003, 14:26:51 ; Search time 1209.27 Seconds
(without alignments)
241.069 Million cell updates/sec

Title: US-09-780-929-98
Perfect score: 18
Sequence: 1 aauggccuaucggugcga 18

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 146654

Minimum DB seq length: 0
Maximum DB seq length: 60

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	13.8	76.7	49	17	TA58C07Q	AL455710 T. brucei
c	2	12.4	68.9	50	9	AU183461	AU183461 AU183461
	3	12.2	67.8	37	14	H13124	H13124 yj06d12.r1
c	4	12.2	67.8	50	14	C00960	C00960 HUMGS000331
	5	11.8	65.6	50	9	AU105634	AU105634 AU105634
c	6	11.8	65.6	56	10	AV847604	AV847604 AV847604
	7	11.6	64.4	29	17	AZ800642	AZ800642 2M0058G16
	8	11.6	64.4	55	9	AA863171	AA863171 og91e02.s
c	9	11.2	62.2	30	17	AZ840293	AZ840293 2M0136H17
c	10	11.2	62.2	36	17	AZ605771	AZ605771 1M0427K13
	11	11.2	62.2	37	9	AA931624	AA931624 oo35b08.s
c	12	11.2	62.2	45	17	AZ317769	AZ317769 1M0036O02
	13	11.2	62.2	51	17	BH618002	BH618002 SALK_0383
	14	11.2	62.2	52	9	AA721034	AA721034 nx89h04.s
	15	11.2	62.2	54	17	BH641243	BH641243 1008046D0
c	16	11	61.1	32	17	TA371C10P	AL495613 T. brucei
c	17	11	61.1	58	9	AI221514	AI221514 qg87c10.x
c	18	10.8	60.0	32	13	BJ066180	BJ066180 BJ066180
	19	10.8	60.0	44	17	BH252563	BH252563 SALK_0135
c	20	10.8	60.0	58	9	AI953654	AI953654 wq23g03.x
	21	10.8	60.0	59	17	AL758565	AL758565 Arabidops
c	22	10.6	58.9	27	17	TA208E12P	AL479456 T. brucei
	23	10.6	58.9	38	17	TA244G07P	AL483538 T. brucei
c	24	10.6	58.9	40	9	AI613042	AI613042 ty06h09.x
c	25	10.6	58.9	40	17	AZ511081	AZ511081 1M0355O20
c	26	10.6	58.9	44	17	AZ499581	AZ499581 1M0337N20
c	27	10.6	58.9	46	9	AA455514	AA455514 zx77g01.s
c	28	10.6	58.9	50	9	AU102871	AU102871 AU102871
c	29	10.6	58.9	50	17	AZ777046	AZ777046 2M0011M08
c	30	10.6	58.9	55	17	BH810903	BH810903 SALK_0566
	31	10.6	58.9	56	14	H42612	H42612 yp13d08.r1
	32	10.6	58.9	58	17	BH256481	BH256481 KG03591-5
	33	10.4	57.8	27	17	AQ025667	AQ025667 l(2)08717
c	34	10.4	57.8	52	9	AA485733	AA485733 zx91e11.s
c	35	10.2	56.7	33	12	BF026570	BF026570 601672580
c	36	10.2	56.7	34	9	AI192963	AI192963 qe68h01.x
	37	10.2	56.7	35	17	TA177A10Q	AL474953 T. brucei
	38	10.2	56.7	36	17	BH751662	BH751662 SALK_0504
	39	10.2	56.7	36	17	BH751810	BH751810 SALK_0506
	40	10.2	56.7	38	17	BH611852	BH611852 SALK_0317
	41	10.2	56.7	38	17	BH618406	BH618406 SALK_0390
	42	10.2	56.7	38	17	BH618437	BH618437 SALK_0390
	43	10.2	56.7	38	17	BH618558	BH618558 SALK_0392
	44	10.2	56.7	38	17	BH751595	BH751595 SALK_0503
	45	10.2	56.7	39	13	BI838507	BI838507 603083494

ALIGNMENTS

RESULT 1
TA58C07Q
LOCUS TA58C07Q 49 bp DNA linear GSS 13-DEC-2000
DEFINITION T. brucei sheared genomic DNA clone 58c07, reverse sequence, genomic survey sequence.
ACCESSION AL455710
VERSION AL455710.1 GI:11857988
KEYWORDS GSS.
SOURCE Trypanosoma brucei.
ORGANISM Trypanosoma brucei
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
REFERENCE 1 (bases 1 to 49)
AUTHORS Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R., Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L., Melville,S.E., Rajandream,M.A. and Barrell,B.G.
TITLE Direct Submission
JOURNAL Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and nhl@sanger.ac.uk
COMMENT Constructed at the Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a cloned population of Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared to give a tight size distribution (
4 kb). The v + i method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.

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          Barrell, Oxford University Press, 1999).
          Email: nelsayed@tigr.org
          Details of T. brucei sequencing at the Sanger Centre are available
          at http://www.sanger.ac.uk/Projects/T_brucei/.
FEATURES             Location/Qualifiers
     source          1. .49
                     /organism="Trypanosoma brucei"
                     /strain="TREU927"
                     /db_xref="taxon:5691"
                     /clone="58c07"
BASE COUNT       15 a     11 c     14 g      9 t
ORIGIN

  Query Match            76.7%;  Score 13.8;  DB 17;  Length 49;
  Best Local Similarity  70.6%;  Pred. No. 7.7e+03;
  Matches   12;  Conservative    3;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 AUGGCCUAUCGGUGCGA 18
              |: ||| |:|||:|||| 
Db         29 ATAGCCGATCGGTGCGA 45


RESULT 2
AU183461/c
LOCUS       AU183461                 50 bp    mRNA    linear   EST 30-JUL-2002
DEFINITION  AU183461 Cyprinus carpio head kidney stimulated by
            lipo-polysaccharide and concanavalin-A Cyprinus carpio cDNA clone
            H119, mRNA sequence.
ACCESSION   AU183461
VERSION     AU183461.1  GI:13919202
KEYWORDS    EST.
SOURCE      common carp.
  ORGANISM  Cyprinus carpio
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes
            ; Cyprinidae; Cyprinus.
REFERENCE   1  (bases 1 to 50)
  AUTHORS   Savan,R. and Sakai,M.
  TITLE     Analysis of expressed sequence tags (EST) obtained from common carp
            , Cyprinus carpio L., head kidney cells after stimulation by two
            mitogens, lipopolysaccharide and concanavalin-A
  JOURNAL   Comp. Biochem. Physiol. B, Biochem. Mol. Biol. 131 (1), 71-82 (2002
            )
  MEDLINE   21607774
COMMENT     Contact: Masahiro Sakai
            Faculty of Agriculture
            Miyazaki University
            1-1 nishi gakuenkibanadai, Miyazaki, Miyazaki 889-2192, Japan
            Email: m.sakai@cc.miyazaki-u.ac.jp.
FEATURES             Location/Qualifiers
     source          1. .50
                     /organism="Cyprinus carpio"
                     /db_xref="taxon:7962"
                     /clone="H119"
                     /clone_lib="Cyprinus carpio head kidney stimulated by
                     lipo-polysaccharide and concanavalin-A"
                     /tissue_type="head kidney"
                     /note="common name:common carp ; stimulated by
                     lipo-polysaccharide and concanavalin-A"
BASE COUNT        9 a     11 c     19 g     11 t
ORIGIN

  Query Match            68.9%;  Score 12.4;  DB 9;  Length 50;
  Best Local Similarity  78.6%;  Pred. No. 3.7e+04;
  Matches   11;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          5 GCCUAUCGGUGCGA 18
              ||| |:|||:|||| 
Db         50 GCCCATCGGTGCGA 37


RESULT 3
H13124
LOCUS       H13124                   37 bp    mRNA    linear   EST 27-JUN-1995
DEFINITION  yj06d12.r1 Soares placenta Nb2HP Homo sapiens cDNA clone
            IMAGE:147959 5' similar to gb:U03486_cds1 GAP JUNCTION ALPHA-5
            PROTEIN (HUMAN);, mRNA sequence.
ACCESSION   H13124
VERSION     H13124.1  GI:877944
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 37)
  AUTHORS   Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman
            ,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J.,
            Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston
            ,R., Williamson,A., Wohldmann,P. and Wilson,R.
  TITLE     The WashU-Merck EST Project
  JOURNAL   Unpublished (1995)
COMMENT     Contact: Wilson RK
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            Insert Size: 1178
            High quality sequence starts: 1
            High quality sequence stops: 1
            Source: IMAGE Consortium, LLNL
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Trace considered overall poor quality
            Insert Length: 1178   Std Error: 0.00
            Seq primer: M13RP1
            High quality sequence stop: 1.
FEATURES             Location/Qualifiers
     source          1. .37
                     /organism="Homo sapiens"
                     /db_xref="GDB:559671"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:147959"
                     /clone_lib="Soares placenta Nb2HP"
                     /sex="Female"
                     /dev_stage="placenta obtained at birth (full term)"
                     /lab_host="DH10B (ampicillin resistant)"
                     /note="Organ: placenta; Vector: pT7T3D (Pharmacia) with a
                     modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
                     strand cDNA was primed with a Not I - oligo(dT) primer [5'
                     AACTGGAAGAATTCGCGGCCGCAGGAATTTTTTTTTTTTTTTTT 3'],
                     double-stranded cDNA was ligated to Eco RI adaptors
                     (Pharmacia), digested with Not I and cloned into the Not I
                     and Eco RI sites of the modified pT7T3 vector. Library
                     went through one round of normalization. Library
                     constructed by Bento Soares and M.Fatima Bonaldo. "
BASE COUNT       10 a      8 c     11 g      6 t      2 others
ORIGIN

  Query Match            67.8%;  Score 12.2;  DB 14;  Length 37;
  Best Local Similarity  58.8%;  Pred. No. 4.3e+04;
  Matches   10;  Conservative    4;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          2 AUGGCCUAUCGGUGCGA 18
              |:| ||:|:| |:| ||
Db         21 ATGACCTATCCGTGTGA 37


RESULT 4
C00960/c
LOCUS       C00960                   50 bp    mRNA    linear   EST 23-JUL-1996
DEFINITION  HUMGS0003315 Human adult (K.Okubo) Homo sapiens cDNA, mRNA
            sequence.
ACCESSION   C00960
VERSION     C00960.1  GI:1433190
KEYWORDS    EST.
```

```
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 50)
  AUTHORS   Okubo,K.
  TITLE     BodyMap; human gene expression database
  JOURNAL   Unpublished (1995)
COMMENT     Contact: Okubo,K.
            Institute for Molecular and Cellular Biol
            Osaka University
            1-3,Yamada-oka, Suita, Osaka Pref. 565, Japan
            Tel: 06-877-5111(ex.3315)
            Email: kousaku@imcb.osaka-u.ac.jp
            Human Gene Signature, 3'-directed cDNA sequence. We are not
            submitting the same cDNA sequence redundantly to DDBJ since 1993.
            For the abundance information of clones with this sequence in this
            library and as well as in other 3'-directed libraries, see '
            http://www.imcb.osaka-u.ac.jp/bodymap'. The sequences of the clones
            represented by this GS sequences is also found there.
FEATURES             Location/Qualifiers
     source          1. .50
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone_lib="Human adult (K.Okubo)"
                     /dev_stage="adult"
                     /note="Organ: blood; Vector: l-gt-11; Site_1: Eco-RI;
                     Monocytes were prepared from blood by ficoll-hypaque,
                     percoll  and T cell rosetting purification steps (purity:
                     96 %). mRNA was prepared from  activated monocytes from a
                     patient with rheumatoid arthritis. mRNA was reverse
                     transcribed with MuLV. Using Eco-RI linkers cDNA was
                     cloned into l-gt-11  vector arms. The cDNA library was
                     screened by differential hybidization  using radioactively
                     marked ss-cDNA from activated and non-activated
                     monocytes.  "
BASE COUNT       11 a     11 c     12 g     15 t      1 others
ORIGIN

  Query Match             67.8%;  Score 12.2;  DB 14;  Length 50;
  Best Local Similarity   64.7%;  Pred. No. 4.6e+04;
  Matches   11;  Conservative    3;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 AAUGGCCUAUCGGUGCG 17
              ||:|||| :|| :|||
Db         34 AATGGCCCCTCGATGCG 18


RESULT 5
AU105634
LOCUS       AU105634                 50 bp    mRNA    linear   EST 30-AUG-2001
DEFINITION  AU105634 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
            KAT08740, mRNA sequence.
ACCESSION   AU105634
VERSION     AU105634.1  GI:13555155
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 50)
  AUTHORS   Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J., Hata
            ,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K., Sakaki
            ,Y., Nakamura,Y., Suyama,A. and Sugano,S.
  TITLE     Diverse transcriptional initiation revealed by fine, large-scale
            mapping of mRNA start sites
  JOURNAL   EMBO Rep. 2 (5), 388-393 (2001)
  MEDLINE   21270072
COMMENT     Contact: Yutaka Suzuki
            Department of Virology
            Institute of Medical Science, University of Tokyo
            4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
            Email: ysuzuki@ims.u-tokyo.ac.jp
            Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano
            ,S. Construction and characterization of a full length-enriched and
            a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).
FEATURES             Location/Qualifiers
     source          1. .50
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="KAT08740"
                     /clone_lib="Sugano Homo sapiens cDNA library"
                     /note="Differential display comparison of untreated and
                     dimethylfumarate treated U937 cells"
BASE COUNT       10 a     14 c     14 g     12 t
ORIGIN

  Query Match             65.6%;  Score 11.8;  DB 9;  Length 50;
  Best Local Similarity   66.7%;  Pred. No. 7.2e+04;
  Matches   10;  Conservative    3;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          4 GGCCUAUCGGUGCGA 18
              ||| :|:| |:||||
Db         20 GGCGTATCCGTGCGA 34


RESULT 6
AV847604/c
LOCUS       AV847604                 56 bp    mRNA    linear   EST 08-NOV-2001
DEFINITION  AV847604 Nori Satoh unpublished cDNA library, larva Ciona
            intestinalis cDNA clone rcilv08b14 3', mRNA sequence.
ACCESSION   AV847604
VERSION     AV847604.1  GI:16828139
KEYWORDS    EST.
SOURCE      Ciona intestinalis.
  ORGANISM  Ciona intestinalis
            Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
            Phlebobranchia; Cionidae; Ciona.
REFERENCE   1  (bases 1 to 56)
  AUTHORS   Satoh,N., Satou,Y., Kohara,Y. and Shin-i,T.
  TITLE     Expressed genes in Ciona intestinalis
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Nori Satoh
            Department of Zoology
            Kyoto University
            Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
            Tel: 81-75-753-4081
            Fax: 81-75-705-1113
            Email: satoh@ascidian.zool.kyoto-u.ac.jp.
FEATURES             Location/Qualifiers
     source          1. .56
                     /organism="Ciona intestinalis"
                     /db_xref="taxon:7719"
                     /clone="rcilv08b14"
                     /clone_lib="Nori Satoh unpublished cDNA library, larva"
                     /tissue_type="whole animal"
                     /dev_stage="larva"
                     /note="Vector: pBluescript SK"
BASE COUNT       12 a     11 c     18 g     15 t
ORIGIN

  Query Match             65.6%;  Score 11.8;  DB 10;  Length 56;
  Best Local Similarity   73.3%;  Pred. No. 7.4e+04;
  Matches   11;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 AUGGCCUAUCGGUGC 16
              |:|||| | |||:||
Db         45 ATGGCCCAACGGTGC 31


RESULT 7
AZ800642
LOCUS       AZ800642                 29 bp    DNA     linear   GSS 16-FEB-2001
DEFINITION  2M0058G16R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC2M0058G16 R, DNA sequence.
ACCESSION   AZ800642
```

```
VERSION     AZ800642.1  GI:12952965
KEYWORDS    GSS.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 29)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
            ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
            and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0058  row: G  column: 16
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 29.
FEATURES             Location/Qualifiers
     source          1. .29
                     /organism="Mus musculus"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC2M0058G16"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."
BASE COUNT        4 a      5 c      7 g     13 t
ORIGIN

  Query Match             64.4%;  Score 11.6;  DB 17;  Length 29;
  Best Local Similarity   61.1%;  Pred. No. 7.8e+04;
  Matches   11;  Conservative    3;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 AAUGGCCUAUCGGUGCGA 18
              | :||||:|: || || |
Db          2 ATTGGCCTATGGGGGCCA 19


RESULT 8
AA863171
LOCUS       AA863171                 55 bp    mRNA    linear   EST 29-APR-1998
DEFINITION  og91e02.s1 NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1455674 3'
            similar to SW:H1E3_HUMAN Q15738 H105E3 PROTEIN. ;, mRNA sequence.
ACCESSION   AA863171
```

```
VERSION     AA863171.1  GI:2955650
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 55)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
            Emmert-Buck, M.D., Ph.D.
             cDNA Library Preparation: M. Bento Soares, Ph.D.
             cDNA Library Arrayed by: Greg Lennon, Ph.D.
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html

            Trace considered overall poor quality
            Insert Length: 360   Std Error: 0.00
            Seq primer: -40m13 fwd. ET from Amersham
            High quality sequence stop: 1.
FEATURES             Location/Qualifiers
     source          1. .55
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:1455674"
                     /clone_lib="NCI_CGAP_Kid5"
                     /tissue_type="2 pooled tumors (clear cell type)"
                     /lab_host="DH10B"
                     /note="Organ: kidney; Vector: pT7T3D-Pac (Pharmacia) with
                     a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
                     strand cDNA was primed with a Not I - oligo(dT) primer [5'
                     AACTGGAAGAATTCGCGGCCGCAATATTTTTTTTTTTTTTTTT 3'],
                     double-stranded cDNA was ligated to Eco RI adaptors
                     (Pharmacia), digested with Not I and cloned into the Not I
                     and Eco RI sites of the modified pT7T3 vector. Library
                     went through one round of normalization. Library
                     constructed by Bento Soares and M. Fatima Bonaldo.  "
BASE COUNT       12 a     16 c     15 g     12 t
ORIGIN

  Query Match             64.4%;  Score 11.6;  DB 9;  Length 55;
  Best Local Similarity   66.7%;  Pred. No. 9.2e+04;
  Matches   12;  Conservative    2;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 AAUGGCCUAUCGGUGCGA 18
              ||: ||| | | |:||||
Db         28 AATTGCCAACCAGTGCGA 45


RESULT 9
AZ840293/c
LOCUS       AZ840293                 30 bp    DNA     linear   GSS 20-FEB-2001
DEFINITION  2M0136H17R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC2M0136H17 R, DNA sequence.
ACCESSION   AZ840293
VERSION     AZ840293.1  GI:13010201
KEYWORDS    GSS.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 30)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
            ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
            and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
```

```
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0136  row: H  column: 17
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 30.
FEATURES              Location/Qualifiers
     source           1. .30
                      /organism="Mus musculus"
                      /strain="C57BL/6J"
                      /db_xref="taxon:10090"
                      /clone="UUGC2M0136H17"
                      /clone_lib="Mouse 10kb plasmid UUGC1M library"
                      /sex="Male"
                      /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                      /note="Vector: PWD42nv; Purified genomic DNA from M.
                      musculus C57BL/6J (male) was obtained  from the Jackson
                      Laboratory Mouse DNA Resource
                      (http://www.jax.org/resources/documents/dnares/). The DNA
                      was hydrodynamically sheared by repeated passage through a
                      0.005 inch orifice at constant velocity. The sheared DNA
                      was blunt end-repaired with T4 DNA polymerase and T4
                      polynucleotide kinase. Adaptor oligonucleotides were
                      ligated to the blunt ends in high  molar excess. The
                      adaptored DNA was purified and size-selected for a 9.5 to
                      10.5 kb range using preparative agarose gel
                      electrophoresis. Vector DNA was prepared from a derivative
                      of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                      inducible derivative of plasmid R1. The vector was ligated
                      with adaptors complementary to the insert adaptors and
                      purified. The sheared, adaptored mouse DNA was annealed to
                      adaptored vector DNA, and transformed into
                      chemically-competent E. coli XL10-Gold (Stratagene) cells
                      and selected for ampicillin resistance."
BASE COUNT        4 a     10 c      9 g      7 t
ORIGIN

  Query Match             62.2%;  Score 11.2;  DB 17;  Length 30;
  Best Local Similarity   62.5%;  Pred. No. 1.2e+05;
  Matches   10;  Conservative    3;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 AAUGGCCUAUCGGUGC 16
              ||:||||: :| | ||
Db         30 AATGGCCTGTCCGAGC 15


RESULT 10
AZ605771/c
LOCUS       AZ605771                 36 bp    DNA     linear   GSS 13-DEC-2000
DEFINITION  1M0427K13F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0427K13 F, DNA sequence.
ACCESSION   AZ605771
VERSION     AZ605771.1  GI:11727961
KEYWORDS    GSS.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 36)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
            ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
            and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0427  row: K  column: 13
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 36.
FEATURES              Location/Qualifiers
     source           1. .36
                      /organism="Mus musculus"
                      /strain="C57BL/6J"
                      /db_xref="taxon:10090"
                      /clone="UUGC1M0427K13"
                      /clone_lib="Mouse 10kb plasmid UUGC1M library"
                      /sex="Male"
                      /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                      /note="Vector: PWD42nv; Purified genomic DNA from M.
                      musculus C57BL/6J (male) was obtained  from the Jackson
                      Laboratory Mouse DNA Resource
                      (http://www.jax.org/resources/documents/dnares/). The DNA
                      was hydrodynamically sheared by repeated passage through a
                      0.005 inch orifice at constant velocity. The sheared DNA
                      was blunt end-repaired with T4 DNA polymerase and T4
                      polynucleotide kinase. Adaptor oligonucleotides were
                      ligated to the blunt ends in high  molar excess. The
                      adaptored DNA was purified and size-selected for a 9.5 to
                      10.5 kb range using preparative agarose gel
                      electrophoresis. Vector DNA was prepared from a derivative
                      of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                      inducible derivative of plasmid R1. The vector was ligated
                      with adaptors complementary to the insert adaptors and
                      purified. The sheared, adaptored mouse DNA was annealed to
                      adaptored vector DNA, and transformed into
                      chemically-competent E. coli XL10-Gold (Stratagene) cells
                      and selected for ampicillin resistance."
BASE COUNT       14 a     10 c      5 g      7 t
ORIGIN

  Query Match             62.2%;  Score 11.2;  DB 17;  Length 36;
  Best Local Similarity   56.2%;  Pred. No. 1.3e+05;
  Matches    9;  Conservative    4;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          2 AUGGCCUAUCGGUGCG 17
              |:|| |:|:| |:| |
Db         18 ATGGTCTATCAGTGTG 3


RESULT 11
AA931624
LOCUS       AA931624                 37 bp    mRNA    linear   EST 24-APR-1998
DEFINITION  oo35b08.s1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1568151 3'
            similar to SW:IBA2_HUMAN Q14657 ITBA2 PROTEIN ;, mRNA sequence.
ACCESSION   AA931624
VERSION     AA931624.1  GI:3086010
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 37)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
```

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality
Seq primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 1.

```
FEATURES             Location/Qualifiers
     source          1. .37
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:1568151"
                     /clone_lib="NCI_CGAP_Lu5"
                     /tissue_type="carcinoid"
                     /lab_host="DH10B"
                     /note="Organ: lung; Vector: pT7T3D-Pac (Pharmacia) with a
                     modified polylinker; 1st strand cDNA was prepared from
                     neuroendocrine lung carcinoid, and was then primed with a
                     Not I - oligo(dT) primer. Double-stranded cDNA was ligated
                     to Eco RI adaptors (Pharmacia), digested with Not I and
                     cloned into the Not I and Eco RI sites of the modified
                     pT7T3 vector.  Library is normalized. Library was
                     constructed by Bento Soares and M. Fatima Bonaldo. "
BASE COUNT        7 a     10 c     11 g      9 t
ORIGIN

  Query Match             62.2%;  Score 11.2;  DB 9;  Length 37;
  Best Local Similarity   56.2%;  Pred. No. 1.3e+05;
  Matches    9;  Conservative    4;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 AAUGGCCUAUCGGUGC 16
              ||: |||:|: ||: |
Db         20 AATTGCCTATGGGTCC 35


RESULT 12
AZ317769/c
LOCUS       AZ317769                 45 bp    DNA     linear   GSS 29-SEP-2000
DEFINITION  1M0036O02R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0036O02 R, DNA sequence.
ACCESSION   AZ317769
VERSION     AZ317769.1  GI:10366900
KEYWORDS    GSS.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 45)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
            ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
            and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0036  row: O  column: 02
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 45.
FEATURES             Location/Qualifiers
     source          1. .45
                     /organism="Mus musculus"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0036O02"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."
BASE COUNT       10 a     11 c     12 g     12 t
ORIGIN

  Query Match             62.2%;  Score 11.2;  DB 17;  Length 45;
  Best Local Similarity   56.2%;  Pred. No. 1.4e+05;
  Matches    9;  Conservative    4;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 AAUGGCCUAUCGGUGC 16
              ||:|  |:|:|| :||
Db         37 AATGCTCTATCGATGC 22


RESULT 13
BH618002
LOCUS       BH618002                 51 bp    DNA     linear   GSS 30-JAN-2002
DEFINITION  SALK_038348 Arabidopsis thaliana TDNA insertion lines Arabidopsis
            thaliana genomic clone SALK_038348, DNA sequence.
ACCESSION   BH618002
VERSION     BH618002.1  GI:18428097
KEYWORDS    GSS.
SOURCE      thale cress.
  ORGANISM  Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1  (bases 1 to 51)
  AUTHORS   Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab
            ,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P.
            , Zimmerman,J. and Ecker,J.R.
  TITLE     A Sequence-Indexed Library of Insertion Mutations in the
            Arabidopsis Genome
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Joseph R. Ecker
            Salk Institute Genomic Analysis Laboratory (SIGnAL)
            The Salk Institute for Biological Studies
            10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
            Tel: 858 453 4100 x1752
            Fax: 858 558 6379
            Email: ecker@salk.edu
            This is single pass sequence recovered from the left border of
            TDNA.
            Class: TDNA tagged.
FEATURES             Location/Qualifiers
     source          1. .51
```

```
                     /organism="Arabidopsis thaliana"
                     /strain="Columbia 0"
                     /db_xref="taxon:3702"
                     /clone="SALK_038348"
                     /clone_lib="Arabidopsis thaliana TDNA insertion lines"
                     /note="PCR was performed on Arabidopsis thaliana lines
                     each of which contains  one or more TDNA insertion
                     elements. The resultant fragment for each  line was
                     directly sequenced to determine the genomic sequence at
                     the  site of insertion. Details of the protocols used can
                     be found at  http://signal.salk.edu/tdna_protocols.html"
BASE COUNT       10 a     15 c     17 g      9 t
ORIGIN

  Query Match             62.2%;  Score 11.2;  DB 17;  Length 51;
  Best Local Similarity   56.2%;  Pred. No. 1.4e+05;
  Matches    9;  Conservative    4;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          3 UGGCCUAUCGGUGCGA 18
              :| ||:|: ||:| ||
Db         29 TGCCCTATAGGTGGGA 44


RESULT 14
AA721034
LOCUS       AA721034                 52 bp    mRNA    linear   EST 22-JAN-1998
DEFINITION  nx89h04.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1269463 3'
            similar to WP:F56D1.3 CE01971 ;, mRNA sequence.
ACCESSION   AA721034
VERSION     AA721034.1  GI:2737169
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 52)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman,
            Ph.D., Gerald Marti, M.D.
             cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
            Bonaldo, Ph.D.
             cDNA Library Arrayed by: Greg Lennon, Ph.D.
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html
            Insert Length: 730   Std Error: 0.00
            Seq primer: -40m13 fwd. ET from Amersham
            High quality sequence stop: 1.
FEATURES             Location/Qualifiers
     source          1. .52
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:1269463"
                     /clone_lib="NCI_CGAP_GCB1"
                     /tissue_type="germinal center B cell"
                     /lab_host="DH10B"
                     /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                     polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
                     was prepared from human tonsillar cells enriched for
                     germinal center B cells by flow sorting (CD20+, IgD-),
                     provided by Dr. Louis M. Staudt (NCI), Dr. David Allman
                     (NCI) and Dr. Gerald Marti (CBER).  cDNA synthesis was
                     primed with a Not I - oligo(dT) primer
                     [5'-TGTTACCAATCTGAAGTGGGAGCGGCCGCCTCATTTTTTTTTTTTTTTTT-3'
                     ]. Double-stranded cDNA was ligated to Eco RI adaptors
                     (Pharmacia), digested with Not I and cloned into the Not I
                     and Eco RI sites of the modified pT7T3 vector. Library
                     went through one round of normalization, and was
                     constructed by Bento Soares and M. Fatima Bonaldo."
BASE COUNT       12 a     12 c     21 g      7 t
ORIGIN

  Query Match             62.2%;  Score 11.2;  DB 9;  Length 52;
  Best Local Similarity   68.8%;  Pred. No. 1.4e+05;
  Matches   11;  Conservative    2;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 AAUGGCCUAUCGGUGC 16
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Db         12 AACGGCCGATTGGTGC 27


RESULT 15
BH641243
LOCUS       BH641243                 54 bp    DNA     linear   GSS 14-FEB-2002
DEFINITION  1008046D05.2EL_y1 1008 - RescueMu Grid I Zea mays genomic, DNA
            sequence.
ACCESSION   BH641243
VERSION     BH641243.1  GI:18668929
KEYWORDS    GSS.
SOURCE      Zea mays.
  ORGANISM  Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
            clade; Panicoideae; Andropogoneae; Zea.
REFERENCE   1  (bases 1 to 54)
  AUTHORS   Walbot,V.
  TITLE     Maize genomic sequences found using engineered RescueMu transposon
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Walbot V
            Department of Biological Sciences
            Stanford University
            855 California Ave, Palo Alto, CA 94304, USA
            Tel: 650 723 2227
            Fax: 650 725 8221
            Email: walbot@stanford.edu
            Possible ligation site of ends cut by 2 different endonucleases.
            Reverse complemented post-ligation sequence from source sequence.
            Plate: 1008046  row: 17
            Class: transposon-tagged.
FEATURES             Location/Qualifiers
     source          1. .54
                     /organism="Zea mays"
                     /cultivar="mixed background W23/A188/B73"
                     /db_xref="taxon:4577"
                     /clone_lib="1008 - RescueMu Grid I"
                     /tissue_type="leaf"
                     /dev_stage="adult"
                     /lab_host="DH10B"
                     /note="Organ: leaf; Vector: RescueMu (engineered from
                     pBlueScript backbone); Site_1: BamHI; Site_2: BglII;
                     RescueMu is a 4.9 kb, modified maize Mu transposon
                     designed to allow plasmid rescue from total genomic DNA.
                     Mu elements insert preferentially into transcription
                     units. For more information on RescueMu, go to the  web
                     site www.zmdb.iastate.edu and follow the links for
                     'RescueMu.' Grid I was grown at Berkeley in 2001. DNA was
                     extracted from leaf punches,  double digested using BamHI
                     and BglII, and ligated to form circular plasmids.  DH10B
                     cells were transformed and then screened on LB plates with
                     ampicillin."
BASE COUNT       12 a     12 c     17 g     13 t
ORIGIN

  Query Match             62.2%;  Score 11.2;  DB 17;  Length 54;
  Best Local Similarity   68.8%;  Pred. No. 1.4e+05;
  Matches   11;  Conservative    2;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          2 AUGGCCUAUCGGUGCG 17
              |:||||:  ||| |||
Db         31 ATGGCCTTACGGGGCG 46
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Search completed: July 6, 2003, 15:28:29
Job time : 1212.27 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: July 6, 2003, 14:33:06 ; Search time 47.4545 Seconds
(without alignments)
116.326 Million cell updates/sec

Title: US-09-780-929-98
Perfect score: 18
Sequence: 1 aauggccuaucggugcga 18

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 635134

Minimum DB seq length: 0
Maximum DB seq length: 60

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
c	1	12.2	67.8	29	4	US-09-199-637A-144	Sequence 144, App
	2	11.8	65.6	30	1	US-07-997-133-5	Sequence 5, Appli
	3	11.8	65.6	30	5	US-07-997-133-5	Sequence 5, Appli
	4	11.8	65.6	40	4	US-09-626-929-3	Sequence 3, Appli
	5	11.8	65.6	40	4	US-09-484-850-3	Sequence 3, Appli
	6	11.8	65.6	40	4	US-09-408-392-3	Sequence 3, Appli
	7	11.8	65.6	40	4	US-09-626-930-3	Sequence 3, Appli
	8	11.8	65.6	40	4	US-09-626-528-3	Sequence 3, Appli
	9	11.6	64.4	26	1	US-08-054-480-5	Sequence 5, Appli
c	10	11.6	64.4	29	1	US-08-413-803-10	Sequence 10, Appl
c	11	11.6	64.4	29	1	US-08-321-488A-10	Sequence 10, Appl
c	12	11.6	64.4	29	5	PCT-US95-03776-10	Sequence 10, Appl
c	13	11.6	64.4	30	1	US-08-413-803-9	Sequence 9, Appli
c	14	11.6	64.4	30	1	US-08-321-488A-9	Sequence 9, Appli
c	15	11.6	64.4	30	2	US-08-943-915-14	Sequence 14, Appl
c	16	11.6	64.4	30	4	US-08-482-918-36	Sequence 36, Appl
c	17	11.6	64.4	30	4	US-09-224-681-36	Sequence 36, Appl
c	18	11.6	64.4	30	4	US-08-336-728A-36	Sequence 36, Appl
c	19	11.6	64.4	30	5	PCT-US95-03776-9	Sequence 9, Appli
	20	11.6	64.4	41	2	US-08-781-620B-10	Sequence 10, Appl
c	21	11.6	64.4	46	2	US-08-520-678A-15	Sequence 15, Appl
c	22	11.6	64.4	46	4	US-08-897-126-15	Sequence 15, Appl
	23	11.4	63.3	17	2	US-08-292-620A-1886	Sequence 1886, Ap
	24	11.4	63.3	17	2	US-08-292-620A-1977	Sequence 1977, Ap
	25	11.4	63.3	17	3	US-09-071-845-1886	Sequence 1886, Ap
	26	11.4	63.3	17	3	US-09-071-845-1977	Sequence 1977, Ap
	27	11.4	63.3	21	4	US-08-397-220B-24	Sequence 24, Appl
	28	11.4	63.3	21	4	US-08-650-093C-24	Sequence 24, Appl
	29	11.4	63.3	21	4	US-08-823-895A-24	Sequence 24, Appl
	30	11.4	63.3	25	3	US-09-150-133-35	Sequence 35, Appl
	31	11.4	63.3	25	3	US-09-150-141-35	Sequence 35, Appl
	32	11.4	63.3	25	4	US-09-374-493-35	Sequence 35, Appl
	33	11.4	63.3	25	4	US-09-374-824-35	Sequence 35, Appl
	34	11.4	63.3	25	4	US-09-374-492-35	Sequence 35, Appl
	35	11.4	63.3	47	4	US-09-641-638-1095	Sequence 1095, Ap
	36	11.2	62.2	24	5	PCT-US96-09473-7	Sequence 7, Appli
c	37	11.2	62.2	26	2	US-08-805-918-31	Sequence 31, Appl
c	38	11.2	62.2	26	2	US-08-811-028-19	Sequence 19, Appl
c	39	11.2	62.2	30	1	US-08-393-985-26	Sequence 26, Appl
	40	11.2	62.2	30	4	US-09-105-697-11	Sequence 11, Appl
	41	11.2	62.2	30	4	US-09-146-631-11	Sequence 11, Appl
	42	11.2	62.2	33	5	PCT-US96-09473-1	Sequence 1, Appli
	43	11.2	62.2	40	2	US-08-425-684-75	Sequence 75, Appl
	44	11.2	62.2	40	2	US-08-675-502-75	Sequence 75, Appl
	45	11.2	62.2	43	4	US-09-686-179A-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-09-199-637A-144/c
; Sequence 144, Application US/09199637A
; Patent No. 6355411
; GENERAL INFORMATION:
; APPLICANT: Ausubel, Frederick
; APPLICANT: Goodman, Howard M.
; APPLICANT: Rahme, Laurence G.
; APPLICANT: Mahajan-Miklos, Shalina
; APPLICANT: Tan, Man-Wah
; APPLICANT: Cao, Hui
; APPLICANT: Drenkard, Eliana
; APPLICANT: Tsongalis, John
; TITLE OF INVENTION: VIRULENCE-ASSOCIATED NUCLEIC ACID
; TITLE OF INVENTION: SEQUENCES AND USES THEREOF
; FILE REFERENCE: 00786/361002
; CURRENT APPLICATION NUMBER: US/09/199,637A
; CURRENT FILING DATE: 1998-11-25
; PRIOR APPLICATION NUMBER: 60/066,517
; PRIOR FILING DATE: 1997-11-25
; NUMBER OF SEQ ID NOS: 437
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 144
; LENGTH: 29
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-199-637A-144

Query Match 67.8%; Score 12.2; DB 4; Length 29;
Best Local Similarity 64.7%; Pred. No. 2.6e+02;
Matches 11; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

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Qy          1 AAUGGCCUAUCGGUGCG 17
              || ||| :|:|| :|||
Db         19 AACGGCGTATCGTTGCG 3
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RESULT 2
US-07-997-133-5
; Sequence 5, Application US/07997133
; Patent No. 5288855
; GENERAL INFORMATION:
; APPLICANT: Bergonzoni, Laura
; APPLICANT: Mazue, Guy
; APPLICANT: Isacchi, Antonella
; APPLICANT: Roncucci, Romeo
; APPLICANT: Sarmientos, Paolo
; TITLE OF INVENTION: Extracellular Form of the Human
; TITLE OF INVENTION: Fibroblast Growth Factor Receptor
; NUMBER OF SEQUENCES: 8

```
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  OBLON, SPIVAK, McCLELLAND, MAIER & NEUSTADT,
;      ADDRESSEE:  P.C.
;      STREET:  1755 Jefferson Davis Highway, Fourth Floor
;      CITY:  Arlington
;      STATE:  Virginia
;      ZIP:  22202
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/997,133
;      FILING DATE:  28-DEC-1992
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/642,755
;      FILING DATE:  18-JAN-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Oblon, No. 5288855man F.
;      REGISTRATION NUMBER:  24,618
;      REFERENCE/DOCKET NUMBER:  769-226-0
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (703)521-4500
;      TELEFAX:  (703)486-2347
;      TELEX:  248855 OPAT UR
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  30 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  unknown
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-07-997-133-5

  Query Match             65.6%;  Score 11.8;  DB 1;  Length 30;
  Best Local Similarity   73.3%;  Pred. No. 4.4e+02;
  Matches   11;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 AUGGCCUAUCGGUGC 16
              | ||||:| |||:||
Db          1 ACGGCCTAGCGGTGC 15


RESULT 3
US-07-997-133-5
; Sequence 5, Application US/07997133
;  GENERAL INFORMATION:
;    APPLICANT:  Bergonzoni, Laura
;    APPLICANT:  Mazue, Guy
;    APPLICANT:  Isacchi, Antonella
;    APPLICANT:  Roncucci, Romeo
;    APPLICANT:  Sarmientos, Paolo
;    TITLE OF INVENTION:  Extracellular Form of the Human
;    TITLE OF INVENTION:  Fibroblast Growth Factor Receptor
;    NUMBER OF SEQUENCES:  8
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  OBLON, SPIVAK, McCLELLAND, MAIER & NEUSTADT,
;      ADDRESSEE:  P.C.
;      STREET:  1755 Jefferson Davis Highway, Fourth Floor
;      CITY:  Arlington
;      STATE:  Virginia
;      ZIP:  22202
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/997,133
;      FILING DATE:  28-DEC-1992
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/642,755
;      FILING DATE:  18-JAN-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Oblon, Norman F.
;      REGISTRATION NUMBER:  24,618
;      REFERENCE/DOCKET NUMBER:  769-226-0
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (703)521-4500
;      TELEFAX:  (703)486-2347
;      TELEX:  248855 OPAT UR
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  30 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  unknown
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-07-997-133-5

  Query Match             65.6%;  Score 11.8;  DB 5;  Length 30;
  Best Local Similarity   73.3%;  Pred. No. 4.4e+02;
  Matches   11;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 AUGGCCUAUCGGUGC 16
              | ||||:| |||:||
Db          1 ACGGCCTAGCGGTGC 15


RESULT 4
US-09-626-929-3
; Sequence 3, Application US/09626929
; Patent No. 6319714
; GENERAL INFORMATION:
;  APPLICANT: CRAMERI, ANDREAS
;  APPLICANT:  STEMMER, WILLEM P.C.
;  APPLICANT:  MINSHULL, JEREMY
;  APPLICANT:  BASS, STEVEN H.
;  APPLICANT:  WELCH, MARK
;  APPLICANT:  NESS, JON E.
;  APPLICANT:  GUSTAFSSON, CLAES
;  APPLICANT:  PATTEN, PHILLIP A.
;  TITLE OF INVENTION: OLIGONUCLEOTIDE MEDIATED NUCLEIC ACID RECOMBINATION
;  FILE REFERENCE: 02-029620US
;  CURRENT APPLICATION NUMBER: US/09/626,929
;    2000-07-27
;  CURRENT FILING DATE:  2000-07-27
;  PRIOR APPLICATION NUMBER: 09/408,392
;  PRIOR FILING DATE: 1999-09-28
;  PRIOR APPLICATION NUMBER: 60/118,813
;  PRIOR FILING DATE: 1999-02-05
;  PRIOR APPLICATION NUMBER: 60/141,049
;  PRIOR FILING DATE: 1999-06-24
;  NUMBER OF SEQ ID NOS: 26
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
;   LENGTH: 40
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Bridging
;   OTHER INFORMATION: oligonucleotides
US-09-626-929-3

  Query Match             65.6%;  Score 11.8;  DB 4;  Length 40;
  Best Local Similarity   60.0%;  Pred. No. 4.6e+02;
  Matches    9;  Conservative    4;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 AAUGGCCUAUCGGUG 15
              | :||| :|:|||:|
Db          6 ACTGGCGTATCGGTG 20
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RESULT 5
US-09-484-850-3
; Sequence 3, Application US/09484850
; Patent No. 6368861
; GENERAL INFORMATION:
;  APPLICANT: CRAMERI, ANDREAS
;  APPLICANT:  STEMMER, WILLEM P.C.
;  APPLICANT:  MINSHULL, JEREMY
;  APPLICANT:  BASS, STEVEN H.
;  APPLICANT:  WELCH, MARK
;  APPLICANT:  NESS, JON E.
;  APPLICANT:  GUSTAFSSON, CLAES
;  APPLICANT:  PATTEN, PHILLIP A.
;  TITLE OF INVENTION: OLIGONUCLEOTIDE MEDIATED NUCLEIC ACID RECOMBINATION
;  FILE REFERENCE: 02-029630US
;  CURRENT APPLICATION NUMBER: US/09/484,850
;  CURRENT FILING DATE:  2000-01-18
;  PRIOR APPLICATION NUMBER: 09/408,392
;  PRIOR FILING DATE: 1999-09-28
;  PRIOR APPLICATION NUMBER: 60/118,813
;  PRIOR FILING DATE: 1999-02-05
;  PRIOR APPLICATION NUMBER: 60/141,049
;  PRIOR FILING DATE: 1999-06-24
;  NUMBER OF SEQ ID NOS: 26
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
;   LENGTH: 40
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Bridging
;   OTHER INFORMATION: oligonucleotides
US-09-484-850-3

  Query Match           65.6%;  Score 11.8;  DB 4;  Length 40;
  Best Local Similarity  60.0%;  Pred. No. 4.6e+02;
  Matches    9;  Conservative    4;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 AAUGGCCUAUCGGUG 15
              | :||| :|:|||:|
Db          6 ACTGGCGTATCGGTG 20


RESULT 6
US-09-408-392-3
; Sequence 3, Application US/09408392
; Patent No. 6376246
; GENERAL INFORMATION:
;  APPLICANT:  CRAMERI, ANDREAS
;  APPLICANT:  STEMMER, WILLEM P.C.
;  APPLICANT:  MINSHULL, JEREMY
;  APPLICANT:  BASS, STEVEN H.
;  APPLICANT:  WELCH, MARK
;  APPLICANT:  NESS, JON E.
;  APPLICANT:  GUSTAFSSON, CLAES
;  APPLICANT:  PATTEN, PHILLIP A.
;  TITLE OF INVENTION:  OLIGONUCLEOTIDE MEDIATED NUCLEIC ACID RECOMBINATION
;  FILE REFERENCE:  02-029620US
;  CURRENT APPLICATION NUMBER: US/09/408,392
;  CURRENT FILING DATE:  1999-09-28
;  PRIOR APPLICATION NUMBER:  60/118,813
;  PRIOR FILING DATE:  1999-02-05
;  PRIOR APPLICATION NUMBER:  60/141,049
;  PRIOR FILING DATE:  1999-06-24
;  NUMBER OF SEQ ID NOS:  26
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 3
;   LENGTH: 40
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Bridging
;   OTHER INFORMATION: oligonucleotides
US-09-408-392-3

  Query Match           65.6%;  Score 11.8;  DB 4;  Length 40;
  Best Local Similarity  60.0%;  Pred. No. 4.6e+02;
  Matches    9;  Conservative    4;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 AAUGGCCUAUCGGUG 15
              | :||| :|:|||:|
Db          6 ACTGGCGTATCGGTG 20


RESULT 7
US-09-626-930-3
; Sequence 3, Application US/09626930
; Patent No. 6423542
; GENERAL INFORMATION:
;  APPLICANT: CRAMERI, ANDREAS
;  APPLICANT:  STEMMER, WILLEM P.C.
;  APPLICANT:  MINSHULL, JEREMY
;  APPLICANT:  BASS, STEVEN H.
;  APPLICANT:  WELCH, MARK
;  APPLICANT:  NESS, JON E.
;  APPLICANT:  GUSTAFSSON, CLAES
;  APPLICANT:  PATTEN, PHILLIP A.
;  TITLE OF INVENTION: OLIGONUCLEOTIDE MEDIATED NUCLEIC ACID RECOMBINATION
;  FILE REFERENCE: 02-029620US
;  CURRENT APPLICATION NUMBER: US/09/626,930
;  CURRENT FILING DATE:  2000-07-27
;  PRIOR APPLICATION NUMBER: 09/408,392
;  PRIOR FILING DATE: 1999-09-28
;  PRIOR APPLICATION NUMBER: 60/118,813
;  PRIOR FILING DATE: 1999-02-05
;  PRIOR APPLICATION NUMBER: 60/141,049
;  PRIOR FILING DATE: 1999-06-24
;  NUMBER OF SEQ ID NOS: 26
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
;   LENGTH: 40
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Bridging
;   OTHER INFORMATION: oligonucleotides
US-09-626-930-3

  Query Match           65.6%;  Score 11.8;  DB 4;  Length 40;
  Best Local Similarity  60.0%;  Pred. No. 4.6e+02;
  Matches    9;  Conservative    4;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 AAUGGCCUAUCGGUG 15
              | :||| :|:|||:|
Db          6 ACTGGCGTATCGGTG 20


RESULT 8
US-09-626-528-3
; Sequence 3, Application US/09626528
; Patent No. 6426224
; GENERAL INFORMATION:
;  APPLICANT: CRAMERI, ANDREAS
;  APPLICANT:  STEMMER, WILLEM P.C.
;  APPLICANT:  MINSHULL, JEREMY
;  APPLICANT:  BASS, STEVEN H.
;  APPLICANT:  WELCH, MARK
;  APPLICANT:  NESS, JON E.
;  APPLICANT:  GUSTAFSSON, CLAES
;  APPLICANT:  PATTEN, PHILLIP A.
;  TITLE OF INVENTION: OLIGONUCLEOTIDE MEDIATED NUCLEIC ACID RECOMBINATION
;  FILE REFERENCE: 02-029620US
;  CURRENT APPLICATION NUMBER: US/09/626,528
;  CURRENT FILING DATE:  2000-07-27
;  PRIOR APPLICATION NUMBER: 09/408,392
;  PRIOR FILING DATE: 1999-09-28
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;  PRIOR APPLICATION NUMBER: 60/118,813
;  PRIOR FILING DATE: 1999-02-05
;  PRIOR APPLICATION NUMBER: 60/141,049
;  PRIOR FILING DATE: 1999-06-24
;  NUMBER OF SEQ ID NOS: 26
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
;   LENGTH: 40
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Bridging
;   OTHER INFORMATION: oligonucleotides
US-09-626-528-3

  Query Match            65.6%;  Score 11.8;  DB 4;  Length 40;
  Best Local Similarity  60.0%;  Pred. No. 4.6e+02;
  Matches    9;  Conservative    4;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 AAUGGCCUAUCGGUG 15
              | :||| :|:|||:|
Db          6 ACTGGCGTATCGGTG 20


RESULT 9
US-08-054-480-5
; Sequence 5, Application US/08054480
; Patent No. 5525504
;  GENERAL INFORMATION:
;    APPLICANT:  Goebel, Werner
;    APPLICANT:  Libby, Stephen
;    APPLICANT:  Heffron, Fred
;    TITLE OF INVENTION:  CYTOLYSIN GENE AND GENE PRODUCT
;    NUMBER OF SEQUENCES:  5
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  MILLEN, WHITE, ZELANO, & BRANIGAN, P.C.
;      STREET:  2200 CLARENDON BOULEVARD, SUITE 1400
;      CITY:  ARLINGTON
;      STATE:  VIRGINIA
;      COUNTRY:  USA
;      ZIP:  22201
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/054,480
;      FILING DATE:  04-APR-1993
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Heaney, Brion P.
;      REGISTRATION NUMBER:  32,542
;      REFERENCE/DOCKET NUMBER:  MERCK 1496
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  703 243 6333
;      TELEFAX:  703 243 6410
;      TELEX:  64191
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  26 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    ORIGINAL SOURCE:
;      ORGANISM:  SALMONELLA
US-08-054-480-5

  Query Match            64.4%;  Score 11.6;  DB 1;  Length 26;
  Best Local Similarity  66.7%;  Pred. No. 5.7e+02;
  Matches   12;  Conservative    2;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 AAUGGCCUAUCGGUGCGA 18
              ||:|||  |  ||:||||
Db          7 AATGGCAGAGAGGTGCGA 24


RESULT 10
US-08-413-803-10/c
; Sequence 10, Application US/08413803
; Patent No. 5766581
;  GENERAL INFORMATION:
;    APPLICANT:  Bartley, Timothy D.
;    APPLICANT:  Bogenberger, Jakob M.
;    APPLICANT:  Bosselman, Robert A.
;    APPLICANT:  Hunt, Pamela
;    APPLICANT:  Kinstler, Olaf B.
;    APPLICANT:  Samal, Babru B.
;    TITLE OF INVENTION:  METHODS FOR TREATING MAMMALS WITH
;    TITLE OF INVENTION:  MONO-PEGYLATED PROTEINS THAT STIMULATE MEGAKARYOCYTE
;    TITLE OF INVENTION:  GROWTH AND DIFFERENTIATION
;    NUMBER OF SEQUENCES:  34
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  AMGEN INC.
;      STREET:  1840 DeHavilland Drive
;      CITY:  Thousand Oaks
;      STATE:  California
;      COUNTRY:  US
;      ZIP:  91320-1789
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/413,803
;      FILING DATE:  30-MAR-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/221,768
;      FILING DATE:  31-MAR-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/252,628
;      FILING DATE:  31-MAY-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/321,488
;      FILING DATE:  12-OCT-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/347,780
;      FILING DATE:  30-NOV-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Cook Ph.D., Robert R.
;      REGISTRATION NUMBER:  31,602
;      REFERENCE/DOCKET NUMBER:  A-290D
;  INFORMATION FOR SEQ ID NO:  10:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  29 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-08-413-803-10

  Query Match            64.4%;  Score 11.6;  DB 1;  Length 29;
  Best Local Similarity  66.7%;  Pred. No. 5.8e+02;
  Matches   12;  Conservative    2;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 AAUGGCCUAUCGGUGCGA 18
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Db         19 AAAGGCCTATCCGGCCGA 2


RESULT 11
US-08-321-488A-10/c
; Sequence 10, Application US/08321488A
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; Patent No. 5795569
;  GENERAL INFORMATION:
;    APPLICANT:  Bartley, Timothy D.
;    APPLICANT:  Bogenberger, Jakob M.
;    APPLICANT:  Bosselman, Robert A.
;    APPLICANT:  Hunt, Pamela
;    APPLICANT:  Kinstler, Olaf B.
;    APPLICANT:  Samal, Babru B.
;    TITLE OF INVENTION:  MONO-PEGYLATED PROTEINS THAT STIMULATE
;    TITLE OF INVENTION:  MEGAKARYOCYTE GROWTH AND DIFFERENTIATION
;    NUMBER OF SEQUENCES:  27
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  AMGEN INC.
;      STREET:  1840 DeHavilland Drive
;      CITY:  Thousand Oaks
;      STATE:  California
;      COUNTRY:  US
;      ZIP:  91320-1789
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/321,488A
;      FILING DATE:  12-OCT-1994
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/252,628
;      FILING DATE:  31-MAY-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/221,768
;      FILING DATE:  31-MAR-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Cook, Robert R.
;      REGISTRATION NUMBER:  31,602
;      REFERENCE/DOCKET NUMBER:  A-290B
;  INFORMATION FOR SEQ ID NO:  10:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  29 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-08-321-488A-10

  Query Match             64.4%;  Score 11.6;  DB 1;  Length 29;
  Best Local Similarity   66.7%;  Pred. No. 5.8e+02;
  Matches   12;  Conservative    2;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 AAUGGCCUAUCGGUGCGA 18
              || ||||:|:| |  |||
Db         19 AAAGGCCTATCCGGCCGA 2


RESULT 12
PCT-US95-03776-10/c
; Sequence 10, Application PC/TUS9503776
;  GENERAL INFORMATION:
;    APPLICANT:  AMGEN INC.
;    TITLE OF INVENTION:  Compositions and Methods for Stimulating
;    TITLE OF INVENTION:  Megakaryocyte Growth and Differentiation
;    NUMBER OF SEQUENCES:  34
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Amgen Inc.
;      STREET:  1840 Dehavilland Drive
;      CITY:  Thousand Oaks
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  91320-1789
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/03776
;      FILING DATE:
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Cook, Robert R.
;      REFERENCE/DOCKET NUMBER:  A-290-C
;  INFORMATION FOR SEQ ID NO:  10:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  29 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
PCT-US95-03776-10

  Query Match             64.4%;  Score 11.6;  DB 5;  Length 29;
  Best Local Similarity   66.7%;  Pred. No. 5.8e+02;
  Matches   12;  Conservative    2;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 AAUGGCCUAUCGGUGCGA 18
              || ||||:|:| |  |||
Db         19 AAAGGCCTATCCGGCCGA 2


RESULT 13
US-08-413-803-9/c
; Sequence 9, Application US/08413803
; Patent No. 5766581
;  GENERAL INFORMATION:
;    APPLICANT:  Bartley, Timothy D.
;    APPLICANT:  Bogenberger, Jakob M.
;    APPLICANT:  Bosselman, Robert A.
;    APPLICANT:  Hunt, Pamela
;    APPLICANT:  Kinstler, Olaf B.
;    APPLICANT:  Samal, Babru B.
;    TITLE OF INVENTION:  METHODS FOR TREATING MAMMALS WITH
;    TITLE OF INVENTION:  MONO-PEGYLATED PROTEINS THAT STIMULATE MEGAKARYOCYTE
;    TITLE OF INVENTION:  GROWTH AND DIFFERENTIATION
;    NUMBER OF SEQUENCES:  34
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  AMGEN INC.
;      STREET:  1840 DeHavilland Drive
;      CITY:  Thousand Oaks
;      STATE:  California
;      COUNTRY:  US
;      ZIP:  91320-1789
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/413,803
;      FILING DATE:  30-MAR-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/221,768
;      FILING DATE:  31-MAR-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/252,628
;      FILING DATE:  31-MAY-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/321,488
;      FILING DATE:  12-OCT-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/347,780
;      FILING DATE:  30-NOV-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Cook Ph.D., Robert R.
;      REGISTRATION NUMBER:  31,602
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;       REFERENCE/DOCKET NUMBER:  A-290D
;   INFORMATION FOR SEQ ID NO:  9:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  30 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  cDNA
US-08-413-803-9

  Query Match             64.4%;  Score 11.6;  DB 1;  Length 30;
  Best Local Similarity   66.7%;  Pred. No. 5.8e+02;
  Matches   12;  Conservative    2;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 AAUGGCCUAUCGGUGCGA 18
              || ||||:|:| |  |||
Db         19 AAAGGCCTATCCGGCCGA 2


RESULT 14
US-08-321-488A-9/c
; Sequence 9, Application US/08321488A
; Patent No. 5795569
;  GENERAL INFORMATION:
;    APPLICANT:  Bartley, Timothy D.
;    APPLICANT:  Bogenberger, Jakob M.
;    APPLICANT:  Bosselman, Robert A.
;    APPLICANT:  Hunt, Pamela
;    APPLICANT:  Kinstler, Olaf B.
;    APPLICANT:  Samal, Babru B.
;    TITLE OF INVENTION:  MONO-PEGYLATED PROTEINS THAT STIMULATE
;    TITLE OF INVENTION:  MEGAKARYOCYTE GROWTH AND DIFFERENTIATION
;    NUMBER OF SEQUENCES:  27
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  AMGEN INC.
;      STREET:  1840 DeHavilland Drive
;      CITY:  Thousand Oaks
;      STATE:  California
;      COUNTRY:  US
;      ZIP:  91320-1789
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/321,488A
;      FILING DATE:  12-OCT-1994
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/252,628
;      FILING DATE:  31-MAY-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/221,768
;      FILING DATE:  31-MAR-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Cook, Robert R.
;      REGISTRATION NUMBER:  31,602
;      REFERENCE/DOCKET NUMBER:  A-290B
;  INFORMATION FOR SEQ ID NO:  9:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  30 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-08-321-488A-9

  Query Match             64.4%;  Score 11.6;  DB 1;  Length 30;
  Best Local Similarity   66.7%;  Pred. No. 5.8e+02;
  Matches   12;  Conservative    2;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 AAUGGCCUAUCGGUGCGA 18
              || ||||:|:| |  |||
Db         19 AAAGGCCTATCCGGCCGA 2


RESULT 15
US-08-943-915-14/c
; Sequence 14, Application US/08943915
; Patent No. 5998170
;  GENERAL INFORMATION:
;    APPLICANT:  Itoh, No. 5998170uyuki
;    APPLICANT:  Martin, Frank
;    APPLICANT:  Danilenko, Dimitry
;    TITLE OF INVENTION:  A FIBROBLAST GROWTH FACTOR
;    NUMBER OF SEQUENCES:  33
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Amgen Inc.
;      STREET:  1840 DeHavilland Drive
;      CITY:  Thousand Oaks
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  91320-1789
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/943,915
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Mazza, Richard J.
;      REGISTRATION NUMBER:  27,657
;      REFERENCE/DOCKET NUMBER:  A-469
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  805.447.4112
;      TELEFAX:  805.447.1090
;  INFORMATION FOR SEQ ID NO:  14:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  30 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  other nucleic acid
;      DESCRIPTION:  /desc = "OLIGONUCLEOTIDE"
US-08-943-915-14

  Query Match             64.4%;  Score 11.6;  DB 2;  Length 30;
  Best Local Similarity   66.7%;  Pred. No. 5.8e+02;
  Matches   12;  Conservative    2;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 AAUGGCCUAUCGGUGCGA 18
              || ||||:|:| |  |||
Db         19 AAAGGCCTATCCGGCCGA 2


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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: July 6, 2003, 15:04:31 ; Search time 102 Seconds
(without alignments)
275.469 Million cell updates/sec

Title: US-09-780-929-98
Perfect score: 18
Sequence: 1 aauggccuaucggugcga 18

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1085931 seqs, 780495707 residues

Total number of hits satisfying chosen parameters: 885896

Minimum DB seq length: 0
Maximum DB seq length: 60

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA:*
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2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
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13: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
14: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	18	100.0	18	10	US-09-780-929-98	Sequence 98, Appl
	2	18	100.0	29	10	US-09-780-929-107	Sequence 107, App
c	3	13.8	76.7	30	10	US-09-798-675-7	Sequence 7, Appli
	4	13.8	76.7	30	10	US-09-798-675-8	Sequence 8, Appli
c	5	12.2	67.8	29	9	US-09-975-719-144	Sequence 144, App
	6	11.8	65.6	24	9	US-09-940-185-3899	Sequence 3899, Ap
c	7	11.6	64.4	30	10	US-09-005-243-36	Sequence 36, Appl
c	8	11.6	64.4	30	10	US-09-224-683-36	Sequence 36, Appl
c	9	11.6	64.4	46	9	US-09-880-508-15	Sequence 15, Appl
c	10	11.6	64.4	46	9	US-10-158-314-15	Sequence 15, Appl
c	11	11.6	64.4	50	9	US-09-741-179A-10	Sequence 10, Appl
c	12	11.6	64.4	50	9	US-09-741-179A-14	Sequence 14, Appl
c	13	11.4	63.3	24	9	US-09-940-185-3596	Sequence 3596, Ap
c	14	11.4	63.3	41	10	US-09-759-272B-4	Sequence 4, Appli
	15	11.4	63.3	42	10	US-09-838-386-14	Sequence 14, Appl
c	16	11.4	63.3	45	10	US-09-838-386-13	Sequence 13, Appl
c	17	11.4	63.3	45	10	US-09-838-386-17	Sequence 17, Appl
	18	11.4	63.3	45	10	US-09-838-386-18	Sequence 18, Appl
	19	11.4	63.3	51	9	US-10-211-088-46	Sequence 46, Appl
c	20	11.2	62.2	17	9	US-09-780-533A-633	Sequence 633, App
	21	11.2	62.2	19	9	US-09-796-081-3	Sequence 3, Appli
c	22	11.2	62.2	19	9	US-09-796-081-4	Sequence 4, Appli
c	23	11.2	62.2	22	10	US-09-997-664-85	Sequence 85, Appl
c	24	11.2	62.2	25	9	US-10-098-263B-3120	Sequence 3120, Ap
c	25	11.2	62.2	25	9	US-10-098-263B-12236	Sequence 12236, A
c	26	11.2	62.2	25	9	US-10-098-263B-26400	Sequence 26400, A
c	27	11.2	62.2	25	9	US-10-098-263B-100906	Sequence 100906,
c	28	11.2	62.2	25	9	US-10-098-263B-120820	Sequence 120820,
	29	11.2	62.2	25	9	US-10-098-263B-126689	Sequence 126689,
	30	11.2	62.2	29	9	US-10-062-458-23	Sequence 23, Appl
	31	11.2	62.2	30	12	US-10-053-632-11	Sequence 11, Appl
	32	11.2	62.2	30	12	US-10-052-417-11	Sequence 11, Appl
	33	11.2	62.2	40	10	US-09-245-802-75	Sequence 75, Appl
	34	11.2	62.2	43	10	US-09-728-574-1	Sequence 1, Appli
	35	11.2	62.2	44	9	US-10-062-458-18	Sequence 18, Appl
	36	11.2	62.2	50	9	US-09-741-179A-13	Sequence 13, Appl
	37	11.2	62.2	50	9	US-09-741-179A-15	Sequence 15, Appl
	38	11	61.1	25	9	US-10-098-263B-26098	Sequence 26098, A
c	39	11	61.1	32	10	US-09-919-831-4	Sequence 4, Appli
c	40	10.8	60.0	21	9	US-09-995-529-223	Sequence 223, App
c	41	10.8	60.0	22	10	US-09-815-656-61	Sequence 61, Appl
c	42	10.8	60.0	22	10	US-09-815-656-63	Sequence 63, Appl
	43	10.8	60.0	22	10	US-09-529-063-114	Sequence 114, App
	44	10.8	60.0	24	9	US-09-940-185-1700	Sequence 1700, Ap
c	45	10.8	60.0	24	9	US-09-940-185-3740	Sequence 3740, Ap

ALIGNMENTS

RESULT 1
US-09-780-929-98
; Sequence 98, Application US/09780929
; Patent No. US20020151693A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc
; APPLICANT: Breaker, Ronald
; APPLICANT: Beigelman, Leo
; TITLE OF INVENTION: Nucleic Acid Catalysts with Endonuclease Activity
; FILE REFERENCE: MBHB00-884-H (500/001)
; CURRENT APPLICATION NUMBER: US/09/780,929
; CURRENT FILING DATE: 2001-02-08
; PRIOR APPLICATION NUMBER: US 60/181,360
; PRIOR FILING DATE: 2000-02-08
; NUMBER OF SEQ ID NOS: 126
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 98
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-09-780-929-98

Query Match 100.0%; Score 18; DB 10; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAUGGCCUAUCGGUGCGA 18
||||||||||||||||||
Db 1 AAUGGCCUAUCGGUGCGA 18

RESULT 2
US-09-780-929-107
; Sequence 107, Application US/09780929
; Patent No. US20020151693A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc
; APPLICANT: Breaker, Ronald
; APPLICANT: Beigelman, Leo
; TITLE OF INVENTION: Nucleic Acid Catalysts with Endonuclease Activity

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;  FILE REFERENCE: MBHB00-884-H (500/001)
;  CURRENT APPLICATION NUMBER: US/09/780,929
;  CURRENT FILING DATE:  2001-02-08
;  PRIOR APPLICATION NUMBER: US 60/181,360
;  PRIOR FILING DATE: 2000-02-08
;  NUMBER OF SEQ ID NOS: 126
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 107
;   LENGTH: 29
;   TYPE: RNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  Enzymatic Nucleic Acid
US-09-780-929-107

  Query Match            100.0%;  Score 18;  DB 10;  Length 29;
  Best Local Similarity  100.0%;  Pred. No. 1.1;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AAUGGCCUAUCGGUGCGA 18
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Db          8 AAUGGCCUAUCGGUGCGA 25


RESULT 3
US-09-798-675-7/c
; Sequence 7, Application US/09798675
; Patent No. US20020106798A1
; GENERAL INFORMATION:
;  APPLICANT: Emory University
;  TITLE OF INVENTION: HIV VACCINES
;  FILE REFERENCE: E056 2020
;  CURRENT APPLICATION NUMBER: US/09/798,675
;  CURRENT FILING DATE:  2001-12-11
;  PRIOR APPLICATION NUMBER: US 60/186,364
;  PRIOR FILING DATE: 2000-03-02
;  PRIOR APPLICATION NUMBER: US 60/251,083
;  PRIOR FILING DATE: 2000-12-01
;  NUMBER OF SEQ ID NOS: 24
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7
;   LENGTH: 30
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: primer for site-directed mutagenesis for introducing Cla I site
US-09-798-675-7

  Query Match            76.7%;  Score 13.8;  DB 10;  Length 30;
  Best Local Similarity  64.7%;  Pred. No. 2.5e+02;
  Matches   11;  Conservative    4;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 AUGGCCUAUCGGUGCGA 18
              |:||| :|:|| :||||
Db         25 ATGGCGTATCGATGCGA 9


RESULT 4
US-09-798-675-8
; Sequence 8, Application US/09798675
; Patent No. US20020106798A1
; GENERAL INFORMATION:
;  APPLICANT: Emory University
;  TITLE OF INVENTION: HIV VACCINES
;  FILE REFERENCE: E056 2020
;  CURRENT APPLICATION NUMBER: US/09/798,675
;  CURRENT FILING DATE:  2001-12-11
;  PRIOR APPLICATION NUMBER: US 60/186,364
;  PRIOR FILING DATE: 2000-03-02
;  PRIOR APPLICATION NUMBER: US 60/251,083
;  PRIOR FILING DATE: 2000-12-01
;  NUMBER OF SEQ ID NOS: 24
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8
;   LENGTH: 30
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: primer for site-directed mutagenesis to introduce Cla I site
US-09-798-675-8

  Query Match            76.7%;  Score 13.8;  DB 10;  Length 30;
  Best Local Similarity  64.7%;  Pred. No. 2.5e+02;
  Matches   11;  Conservative    4;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 AUGGCCUAUCGGUGCGA 18
              |:||| :|:|| :||||
Db          6 ATGGCGTATCGATGCGA 22


RESULT 5
US-09-975-719-144/c
; Sequence 144, Application US/09975719
; Publication No. US20030022349A1
; GENERAL INFORMATION:
;  APPLICANT: Ausubel, Frederick M.
;  APPLICANT:  Rahme, Laurence G.
;  TITLE OF INVENTION: VIRULENCE-ASSOCIATED NUCLEIC ACID
;  TITLE OF INVENTION:  SEQUENCES AND USES THEREOF
;  FILE REFERENCE: 00786/361003
;  CURRENT APPLICATION NUMBER: US/09/975,719
;  CURRENT FILING DATE:  2001-10-10
;  PRIOR APPLICATION NUMBER: US 09/199,637
;  PRIOR FILING DATE: 1998-11-25
;  PRIOR APPLICATION NUMBER: US 60/066,517
;  PRIOR FILING DATE: 1997-11-25
;  NUMBER OF SEQ ID NOS: 437
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 144
;   LENGTH: 29
;   TYPE: DNA
;   ORGANISM: Pseudomonas aeruginosa
US-09-975-719-144

  Query Match            67.8%;  Score 12.2;  DB 9;  Length 29;
  Best Local Similarity  64.7%;  Pred. No. 2e+03;
  Matches   11;  Conservative    3;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 AAUGGCCUAUCGGUGCG 17
              || ||| :|:|| :|||
Db         19 AACGGCGTATCGTTGCG 3


RESULT 6
US-09-940-185-3899
; Sequence 3899, Application US/09940185
; Publication No. US20030096239A1
; GENERAL INFORMATION:
;  APPLICANT: Gunderson, Kevin
;  APPLICANT:  Chee, Mark
;  TITLE OF INVENTION: Probes and Decoder Oligonucleotides
;  FILE REFERENCE: A-69605-1
;  CURRENT APPLICATION NUMBER: US/09/940,185
;  CURRENT FILING DATE:  2001-08-27
;  PRIOR APPLICATION NUMBER: US 60/227,948
;  PRIOR FILING DATE: 2000-08-25
;  PRIOR APPLICATION NUMBER: US 60/228,854
;  PRIOR FILING DATE: 2000-08-29
;  NUMBER OF SEQ ID NOS: 4768
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3899
;   LENGTH: 24
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Computer Generated Probe Sequence.
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US-09-940-185-3899

Query Match 65.6%; Score 11.8; DB 9; Length 24;
Best Local Similarity 73.3%; Pred. No. 3.3e+03;
Matches 11; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

```
Qy          4 GGCCUAUCGGUGCGA 18
              ||||:|  ||:|||| 
Db          2 GGCCTAGAGGTGCGA 16
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RESULT 7
US-09-005-243-36/c
; Sequence 36, Application US/09005243
; Patent No. US20020018763A1
; GENERAL INFORMATION:
; APPLICANT: Zsebo, Krisztina M.
; APPLICANT: Bosselman, Robert A.
; APPLICANT: Suggs, Sidney V.
; APPLICANT: Martin, Francis H.
; TITLE OF INVENTION: Stem Cell Factor
; NUMBER OF SEQUENCES: 104
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/005,243
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/449,653
; FILING DATE: 24-MAY-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/982,255
; FILING DATE: 25-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/589,701
; FILING DATE: 01-OCT-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/573,616
; FILING DATE: 24-AUG-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/537,198
; FILING DATE: 11-JUN-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/422,383
; FILING DATE: 16-OCT-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Clough, David W.
; REGISTRATION NUMBER: 36,107
; REFERENCE/DOCKET NUMBER: 01017/34465
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 36:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-09-005-243-36

Query Match 64.4%; Score 11.6; DB 10; Length 30;
Best Local Similarity 66.7%; Pred. No. 4.3e+03;
Matches 12; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

```
Qy          1 AAUGGCCUAUCGGUGCGA 18
              || ||||:|:| |  ||| 
Db         19 AAAGGCCTATCCGGCCGA 2
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RESULT 8
US-09-224-683-36/c
; Sequence 36, Application US/09224683
; Patent No. US20020031491A1
; GENERAL INFORMATION:
; APPLICANT: Zsebo, Krisztina M.
; APPLICANT: Bosselman, Robert A.
; APPLICANT: Suggs, Sidney V.
; APPLICANT: Martin, Francis H.
; TITLE OF INVENTION: Stem Cell Factor: Composition Claims
; NUMBER OF SEQUENCES: 104
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/224,683
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/005,893
; FILING DATE: 12-JAN-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/449,653
; FILING DATE: 24-MAY-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/982,255
; FILING DATE: 25-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/589,701
; FILING DATE: 01-OCT-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/573,616
; FILING DATE: 24-AUG-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/537,198
; FILING DATE: 11-JUN-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/422,383
; FILING DATE: 16-OCT-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Clough, David W.
; REGISTRATION NUMBER: 36,107
; REFERENCE/DOCKET NUMBER: 01017/35136
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 36:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single

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;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA
US-09-224-683-36

  Query Match             64.4%;  Score 11.6;  DB 10;  Length 30;
  Best Local Similarity   66.7%;  Pred. No. 4.3e+03;
  Matches   12;  Conservative    2;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 AAUGGCCUAUCGGUGCGA 18
              || |||:|:| |  |||
Db         19 AAAGGCCTATCCGGCCGA 2


RESULT 9
US-09-880-508-15/c
; Sequence 15, Application US/09880508
; Publication No. US20030027130A1
;   GENERAL INFORMATION:
;        APPLICANT: Rice, Charles M.
;                   Kolykhalov, Alexander A.
;        TITLE OF INVENTION: NOVEL 3' TERMINAL SEQUENCE OF HEPATITIS
;                            C VIRUS GENOME AND DIAGNOSTIC AND THERAPEUTIC USES THEREOF
;        NUMBER OF SEQUENCES: 39
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Howell & Haferkamp, L.C.
;             STREET: 7733 Forsyth Blvd., Suite 1400
;             CITY: St. Louis
;             STATE: MO
;             COUNTRY: USA
;             ZIP: 63105
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/880,508
;             FILING DATE: 13-Jun-2001
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 08/897,126
;             FILING DATE: <Unknown>
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Henderson, Melodie W.
;             REGISTRATION NUMBER: 37,848
;             REFERENCE/DOCKET NUMBER: 6029-6836
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 314-727-5188
;             TELEFAX: 314-727-6092
;             TELEX: <Unknown>
;   INFORMATION FOR SEQ ID NO: 15:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 46 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: DNA (genomic)
;        FEATURE:
;             NAME/KEY:  misc_feature
;             LOCATION:  46
;             OTHER INFORMATION:  /product= "NUCLEOTIDE REPEAT"
;        SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-09-880-508-15

  Query Match             64.4%;  Score 11.6;  DB 9;  Length 46;
  Best Local Similarity   61.1%;  Pred. No. 4.4e+03;
  Matches   11;  Conservative    3;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 AAUGGCCUAUCGGUGCGA 18
              ||:||||:|: ||   ||
Db         37 AATGGCCTATTGGCTGGA 20


RESULT 10
US-10-158-314-15/c
; Sequence 15, Application US/10158314
; Publication No. US20030054341A1
;   GENERAL INFORMATION:
;        APPLICANT: Rice, Charles M.
;                   Kolykhalov, Alexander A.
;        TITLE OF INVENTION: NOVEL 3' TERMINAL SEQUENCE OF HEPATITIS
;                            C VIRUS GENOME AND DIAGNOSTIC AND THERAPEUTIC USES THER
;        NUMBER OF SEQUENCES: 39
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Howell & Haferkamp, L.C.
;             STREET: 7733 Forsyth Blvd., Suite 1400
;             CITY: St. Louis
;             STATE: MO
;             COUNTRY: USA
;             ZIP: 63105
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/158,314
;             FILING DATE: 30-May-2002
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/09/368,958
;             FILING DATE: <Unknown>
;             APPLICATION NUMBER: 08/897,126
;             FILING DATE: <Unknown>
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Henderson, Melodie W.
;             REGISTRATION NUMBER: 37,848
;             REFERENCE/DOCKET NUMBER: 6029-6836
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 314-727-5188
;             TELEFAX: 314-727-6092
;             TELEX: <Unknown>
;   INFORMATION FOR SEQ ID NO: 15:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 46 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: DNA (genomic)
;        FEATURE:
;             NAME/KEY:  misc_feature
;             LOCATION:  46
;             OTHER INFORMATION:  /product= "NUCLEOTIDE REPEAT"
;        SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-10-158-314-15

  Query Match             64.4%;  Score 11.6;  DB 9;  Length 46;
  Best Local Similarity   61.1%;  Pred. No. 4.4e+03;
  Matches   11;  Conservative    3;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 AAUGGCCUAUCGGUGCGA 18
              ||:||||:|: ||   ||
Db         37 AATGGCCTATTGGCTGGA 20


RESULT 11
US-09-741-179A-10/c
; Sequence 10, Application US/09741179A
; Publication No. US20030022164A1
; GENERAL INFORMATION:
;  APPLICANT: MILLS, ALLEN
;  TITLE OF INVENTION: DNA-BASED ANALOG NEURAL NETWORKS
;  FILE REFERENCE: 31860-168252
;  CURRENT APPLICATION NUMBER: US/09/741,179A
;  CURRENT FILING DATE:  2000-12-21
;  PRIOR APPLICATION NUMBER: 09/129,958
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;  PRIOR FILING DATE: 1998-08-06
;  PRIOR APPLICATION NUMBER: 60/293,263
;  PRIOR FILING DATE: 2000-10-12
;  NUMBER OF SEQ ID NOS: 29
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
;   LENGTH: 50
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: illustrative nucleotide sequence
US-09-741-179A-10

  Query Match             64.4%;  Score 11.6;  DB 9;  Length 50;
  Best Local Similarity   55.6%;  Pred. No. 4.4e+03;
  Matches   10;  Conservative    4;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 AAUGGCCUAUCGGUGCGA 18
              | :|| |:|:| |:| ||
Db         45 ATTGGTCTATCTGTGTGA 28


RESULT 12
US-09-741-179A-14/c
; Sequence 14, Application US/09741179A
; Publication No. US20030022164A1
; GENERAL INFORMATION:
;  APPLICANT: MILLS, ALLEN
;  TITLE OF INVENTION: DNA-BASED ANALOG NEURAL NETWORKS
;  FILE REFERENCE: 31860-168252
;  CURRENT APPLICATION NUMBER: US/09/741,179A
;  CURRENT FILING DATE:  2000-12-21
;  PRIOR APPLICATION NUMBER: 09/129,958
;  PRIOR FILING DATE: 1998-08-06
;  PRIOR APPLICATION NUMBER: 60/293,263
;  PRIOR FILING DATE: 2000-10-12
;  NUMBER OF SEQ ID NOS: 29
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
;   LENGTH: 50
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: illustrative nucleotide sequence
US-09-741-179A-14

  Query Match             64.4%;  Score 11.6;  DB 9;  Length 50;
  Best Local Similarity   55.6%;  Pred. No. 4.4e+03;
  Matches   10;  Conservative    4;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 AAUGGCCUAUCGGUGCGA 18
              | :|| |:|:| |:| ||
Db         45 ATTGGTCTATCTGTGTGA 28


RESULT 13
US-09-940-185-3596/c
; Sequence 3596, Application US/09940185
; Publication No. US20030096239A1
; GENERAL INFORMATION:
;  APPLICANT: Gunderson, Kevin
;  APPLICANT:  Chee, Mark
;  TITLE OF INVENTION: Probes and Decoder Oligonucleotides
;  FILE REFERENCE: A-69605-1
;  CURRENT APPLICATION NUMBER: US/09/940,185
;  CURRENT FILING DATE:  2001-08-27
;  PRIOR APPLICATION NUMBER: US 60/227,948
;  PRIOR FILING DATE: 2000-08-25
;  PRIOR APPLICATION NUMBER: US 60/228,854
;  PRIOR FILING DATE: 2000-08-29
;  NUMBER OF SEQ ID NOS: 4768
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3596
;   LENGTH: 24
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Computer Generated Probe Sequence.
US-09-940-185-3596

  Query Match             63.3%;  Score 11.4;  DB 9;  Length 24;
  Best Local Similarity   69.2%;  Pred. No. 5.6e+03;
  Matches    9;  Conservative    3;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          6 CCUAUCGGUGCGA 18
              | :|:|||:||||
Db         24 CATATCGGTGCGA 12


RESULT 14
US-09-759-272B-4/c
; Sequence 4, Application US/09759272B
; Patent No. US20020137111A1
; GENERAL INFORMATION:
;  APPLICANT: Peeling Dr., Rosanna W
;  TITLE OF INVENTION: Chlamydia Heat Shock Protein
;  FILE REFERENCE: 83815-1702
;  CURRENT APPLICATION NUMBER: US/09/759,272B
;  CURRENT FILING DATE:  2001-01-16
;  NUMBER OF SEQ ID NOS: 5
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
;   LENGTH: 41
;   TYPE: DNA
;   ORGANISM: Chlamydia trachomatis
US-09-759-272B-4

  Query Match             63.3%;  Score 11.4;  DB 10;  Length 41;
  Best Local Similarity   52.9%;  Pred. No. 5.7e+03;
  Matches    9;  Conservative    5;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 AAUGGCCUAUCGGUGCG 17
              ||:|| |:|:  ::|||
Db         31 AATGGACTAYTARTGCG 15


RESULT 15
US-09-838-386-14
; Sequence 14, Application US/09838386
; Patent No. US20010055756A1
; GENERAL INFORMATION:
;  APPLICANT: Pellerin, Charles
;  APPLICANT:  Kukolj, George
;  TITLE OF INVENTION: Internal De No. US20010055756A1o Initiation Sites of the HC'
;  TITLE OF INVENTION:  Thereof
;  FILE REFERENCE: 1011.2180001
;  CURRENT APPLICATION NUMBER: US/09/838,386
;  CURRENT FILING DATE:  2001-04-20
;  PRIOR APPLICATION NUMBER: US 60/198,793
;  PRIOR FILING DATE: 2000-04-21
;  NUMBER OF SEQ ID NOS: 25
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 14
;   LENGTH: 42
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: oligonucleotide
US-09-838-386-14

  Query Match             63.3%;  Score 11.4;  DB 10;  Length 42;
  Best Local Similarity   69.2%;  Pred. No. 5.7e+03;
  Matches    9;  Conservative    3;  Mismatches    1;  Indels    0;  Gaps    0;
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Qy          1 AAUGGCCUAUCGG 13
              ||:||||:|: ||
Db         23 AATGGCCTATTGG 35
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Job time : 103 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: July 6, 2003, 14:40:47 ; Search time 1951.09 Seconds
(without alignments)
231.955 Million cell updates/sec

Title: US-09-780-929-98
Perfect score: 18
Sequence: 1 aauggccuaucggugcga 18

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 24791104 seqs, 12571243825 residues

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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26: /cgn2_6/ptodata/1/pna/US096D_COMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	18	100.0	18	30	US-09-780-929-98	Sequence 98, Appl
	2	18	100.0	29	30	US-09-780-929-107	Sequence 107, App
c	3	13.8	76.7	30	1	PCT-US01-06795A-7	Sequence 7, Appli
	4	13.8	76.7	30	1	PCT-US01-06795A-8	Sequence 8, Appli
c	5	13.8	76.7	30	30	US-09-798-675-7	Sequence 7, Appli
	6	13.8	76.7	30	30	US-09-798-675-8	Sequence 8, Appli
	7	13.4	74.4	60	34	US-09-908-975-20491	Sequence 20491, A
	8	13.4	74.4	60	34	US-09-908-975A-20491	Sequence 20491, A
	9	13.4	74.4	60	72	US-60-287-724-20491	Sequence 20491, A
	10	13.2	73.3	25	36	US-09-954-427-30098	Sequence 30098, A
c	11	13.2	73.3	25	36	US-09-956-584-426597	Sequence 426597,
c	12	13.2	73.3	25	36	US-09-956-604-6465	Sequence 6465, Ap
c	13	13.2	73.3	25	36	US-09-956-604-105593	Sequence 105593,
c	14	13.2	73.3	25	36	US-09-956-604-114271	Sequence 114271,
c	15	13.2	73.3	25	36	US-09-956-604A-6465	Sequence 6465, Ap
c	16	13.2	73.3	25	36	US-09-956-604A-105593	Sequence 105593,
c	17	13.2	73.3	25	36	US-09-956-604A-114271	Sequence 114271,
c	18	13.2	73.3	25	36	US-09-956-604B-6465	Sequence 6465, Ap
c	19	13.2	73.3	25	36	US-09-956-604B-105593	Sequence 105593,
c	20	13.2	73.3	25	36	US-09-956-604B-114271	Sequence 114271,
	21	13.2	73.3	25	67	US-60-233-166-30098	Sequence 30098, A

c	22	13.2	73.3	25	67	US-60-234-017-416087	Sequence 416087,
c	23	13.2	73.3	25	67	US-60-234-049-64081	Sequence 64081, A
c	24	13.2	73.3	25	67	US-60-234-049-86809	Sequence 86809, A
c	25	13.2	73.3	25	67	US-60-234-049-101848	Sequence 101848,
	26	13	72.2	25	79	US-60-353-987-821852	Sequence 821852,
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	28	12.8	71.1	25	36	US-09-956-584-317679	Sequence 317679,
	29	12.8	71.1	25	36	US-09-956-584-317685	Sequence 317685,
c	30	12.8	71.1	25	36	US-09-956-584-326308	Sequence 326308,
c	31	12.8	71.1	25	36	US-09-956-584-326311	Sequence 326311,
c	32	12.8	71.1	25	36	US-09-956-584-577343	Sequence 577343,
c	33	12.8	71.1	25	36	US-09-956-604-110553	Sequence 110553,
c	34	12.8	71.1	25	36	US-09-956-604A-110553	Sequence 110553,
c	35	12.8	71.1	25	36	US-09-956-604B-110553	Sequence 110553,
c	36	12.8	71.1	25	67	US-60-233-620-39955	Sequence 39955, A
c	37	12.8	71.1	25	67	US-60-234-017-131964	Sequence 131964,
	38	12.8	71.1	25	67	US-60-234-017-287127	Sequence 287127,
	39	12.8	71.1	25	67	US-60-234-017-287141	Sequence 287141,
c	40	12.8	71.1	25	67	US-60-234-017-376130	Sequence 376130,
c	41	12.8	71.1	25	67	US-60-234-017-376137	Sequence 376137,
c	42	12.8	71.1	25	67	US-60-234-017-547071	Sequence 547071,
c	43	12.8	71.1	25	67	US-60-234-049-122491	Sequence 122491,
	44	12.8	71.1	25	79	US-60-353-987-133076	Sequence 133076,
c	45	12.8	71.1	25	79	US-60-353-987-152466	Sequence 152466,

ALIGNMENTS

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RESULT 1
US-09-780-929-98
; Sequence 98, Application US/09780929
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals, Inc
;  APPLICANT:  Breaker, Ronald
;  APPLICANT:  Beigelman, Leo
;  TITLE OF INVENTION: Nucleic Acid Catalysts with Endonuclease Activity
;  FILE REFERENCE: MBHB00-884-H (500/001)
;  CURRENT APPLICATION NUMBER: US/09/780,929
;  CURRENT FILING DATE:  2001-02-08
;  PRIOR APPLICATION NUMBER: US 60/181,360
;  PRIOR FILING DATE: 2000-02-08
;  NUMBER OF SEQ ID NOS: 126
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 98
;   LENGTH: 18
;   TYPE: RNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  Enzymatic Nucleic Acid
US-09-780-929-98

  Query Match             100.0%;  Score 18;  DB 30;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 7.9;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AAUGGCCUAUCGGUGCGA 18
              ||||||||||||||||||
Db          1 AAUGGCCUAUCGGUGCGA 18


RESULT 2
US-09-780-929-107
; Sequence 107, Application US/09780929
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals, Inc
;  APPLICANT:  Breaker, Ronald
;  APPLICANT:  Beigelman, Leo
;  TITLE OF INVENTION: Nucleic Acid Catalysts with Endonuclease Activity
;  FILE REFERENCE: MBHB00-884-H (500/001)
;  CURRENT APPLICATION NUMBER: US/09/780,929
;  CURRENT FILING DATE:  2001-02-08
;  PRIOR APPLICATION NUMBER: US 60/181,360
;  PRIOR FILING DATE: 2000-02-08
;  NUMBER OF SEQ ID NOS: 126
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 107
;   LENGTH: 29
;   TYPE: RNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  Enzymatic Nucleic Acid
US-09-780-929-107

  Query Match             100.0%;  Score 18;  DB 30;  Length 29;
  Best Local Similarity   100.0%;  Pred. No. 8.2;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AAUGGCCUAUCGGUGCGA 18
              ||||||||||||||||||
Db          8 AAUGGCCUAUCGGUGCGA 25


RESULT 3
PCT-US01-06795A-7/c
; Sequence 7, Application PC/TUS0106795A
; GENERAL INFORMATION:
;  APPLICANT: Emory University
;  TITLE OF INVENTION: HIV VACCINES
;  FILE REFERENCE: E056 2020
;  CURRENT APPLICATION NUMBER: PCT/US01/06795A
;  CURRENT FILING DATE:  2001-03-02
;  PRIOR APPLICATION NUMBER: US 60/186,364
;  PRIOR FILING DATE: 2000-03-02
;  PRIOR APPLICATION NUMBER: US 60/251,083
;  PRIOR FILING DATE: 2000-12-01
;  NUMBER OF SEQ ID NOS: 24
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
;   LENGTH: 30
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: primer for site-directed mutagenesis for introducing Cla I sit
PCT-US01-06795A-7

  Query Match             76.7%;  Score 13.8;  DB 1;  Length 30;
  Best Local Similarity   64.7%;  Pred. No. 2.4e+03;
  Matches   11;  Conservative    4;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 AUGGCCUAUCGGUGCGA 18
              |:||| :|:|| :||||
Db         25 ATGGCGTATCGATGCGA 9


RESULT 4
PCT-US01-06795A-8
; Sequence 8, Application PC/TUS0106795A
; GENERAL INFORMATION:
;  APPLICANT: Emory University
;  TITLE OF INVENTION: HIV VACCINES
;  FILE REFERENCE: E056 2020
;  CURRENT APPLICATION NUMBER: PCT/US01/06795A
;  CURRENT FILING DATE:  2001-03-02
;  PRIOR APPLICATION NUMBER: US 60/186,364
;  PRIOR FILING DATE: 2000-03-02
;  PRIOR APPLICATION NUMBER: US 60/251,083
;  PRIOR FILING DATE: 2000-12-01
;  NUMBER OF SEQ ID NOS: 24
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
;   LENGTH: 30
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: primer for site-directed mutagenesis to introduce Cla I site
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PCT-US01-06795A-8

Query Match 76.7%; Score 13.8; DB 1; Length 30;
Best Local Similarity 64.7%; Pred. No. 2.4e+03;
Matches 11; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

```
Qy          2 AUGGCCUAUCGGUGCGA 18
              |:||| :|:|| :||||
Db          6 ATGGCGTATCGATGCGA 22
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RESULT 5
US-09-798-675-7/c
; Sequence 7, Application US/09798675
; GENERAL INFORMATION:
; APPLICANT: Emory University
; TITLE OF INVENTION: HIV VACCINES
; FILE REFERENCE: E056 2020
; CURRENT APPLICATION NUMBER: US/09/798,675
; CURRENT FILING DATE: 2001-12-11
; PRIOR APPLICATION NUMBER: US 60/186,364
; PRIOR FILING DATE: 2000-03-02
; PRIOR APPLICATION NUMBER: US 60/251,083
; PRIOR FILING DATE: 2000-12-01
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer for site-directed mutagenesis for introducing Cla I site
US-09-798-675-7

Query Match 76.7%; Score 13.8; DB 30; Length 30;
Best Local Similarity 64.7%; Pred. No. 2.4e+03;
Matches 11; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

```
Qy          2 AUGGCCUAUCGGUGCGA 18
              |:||| :|:|| :||||
Db         25 ATGGCGTATCGATGCGA 9
```

RESULT 6
US-09-798-675-8
; Sequence 8, Application US/09798675
; GENERAL INFORMATION:
; APPLICANT: Emory University
; TITLE OF INVENTION: HIV VACCINES
; FILE REFERENCE: E056 2020
; CURRENT APPLICATION NUMBER: US/09/798,675
; CURRENT FILING DATE: 2001-12-11
; PRIOR APPLICATION NUMBER: US 60/186,364
; PRIOR FILING DATE: 2000-03-02
; PRIOR APPLICATION NUMBER: US 60/251,083
; PRIOR FILING DATE: 2000-12-01
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer for site-directed mutagenesis to introduce Cla I site
US-09-798-675-8

Query Match 76.7%; Score 13.8; DB 30; Length 30;
Best Local Similarity 64.7%; Pred. No. 2.4e+03;
Matches 11; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

```
Qy          2 AUGGCCUAUCGGUGCGA 18
              |:||| :|:|| :||||
Db          6 ATGGCGTATCGATGCGA 22
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RESULT 7
US-09-908-975-20491
; Sequence 20491, Application US/09908975
; GENERAL INFORMATION:
; APPLICANT: SHOSHAN, Avi
; APPLICANT: WASSERMAN, Alon
; APPLICANT: MINTZ, Eli
; APPLICANT: MINTZ, Liat
; APPLICANT: FAIGLER, Simchon
; TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SI
; TITLE OF INVENTION: THAT POPULATE A TRANSCRIPTOME
; FILE REFERENCE: 36688-0005
; CURRENT APPLICATION NUMBER: US/09/908,975
; CURRENT FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: US 60/287,724
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: US 60/221,607
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 32337
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 20491
; LENGTH: 60
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-908-975-20491

Query Match 74.4%; Score 13.4; DB 34; Length 60;
Best Local Similarity 66.7%; Pred. No. 4.4e+03;
Matches 10; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

```
Qy          1 AAUGGCCUAUCGGUG 15
              | :||||:|:|||:|
Db          1 ATTGGCCTATCGGTG 15
```

RESULT 8
US-09-908-975A-20491
; Sequence 20491, Application US/09908975A
; GENERAL INFORMATION:
; APPLICANT: SHOSHAN, Avi
; APPLICANT: WASSERMAN, Alon
; APPLICANT: MINTZ, Eli
; APPLICANT: MINTZ, Liat
; APPLICANT: FAIGLER, Simchon
; TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SI
; TITLE OF INVENTION: THAT POPULATE A TRANSCRIPTOME
; FILE REFERENCE: 36688-0006
; CURRENT APPLICATION NUMBER: US/09/908,975A
; CURRENT FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: US 60/287,724
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: US 60/221,607
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 32337
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 20491
; LENGTH: 60
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-908-975A-20491

Query Match 74.4%; Score 13.4; DB 34; Length 60;
Best Local Similarity 66.7%; Pred. No. 4.4e+03;
Matches 10; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

```
Qy          1 AAUGGCCUAUCGGUG 15
              | :||||:|:|||:|
Db          1 ATTGGCCTATCGGTG 15
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RESULT 9

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US-60-287-724-20491
; Sequence 20491, Application US/60287724
; GENERAL INFORMATION:
;  APPLICANT: SHOSHAN, Avi
;  APPLICANT:  WASSERMAN, Alon
;  APPLICANT:  MINTZ, Eli
;  APPLICANT:  MINTZ, Liat
;  APPLICANT:  FAIGLER, Simchon
;  TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLICE
;  TITLE OF INVENTION:  THAT POPULATE A TRANSCRIPTOME
;  FILE REFERENCE: 36688-0004
;  CURRENT APPLICATION NUMBER: US/60/287,724
;  CURRENT FILING DATE:  2001-05-02
;  NUMBER OF SEQ ID NOS: 32337
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 20491
;   LENGTH: 60
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-60-287-724-20491

  Query Match             74.4%;  Score 13.4;  DB 72;  Length 60;
  Best Local Similarity   66.7%;  Pred. No. 4.4e+03;
  Matches   10;  Conservative    4;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 AAUGGCCUAUCGGUG 15
              | :||||:|:|||:|
Db          1 ATTGGCCTATCGGTG 15


RESULT 10
US-09-954-427-30098
; Sequence 30098, Application US/09954427
; GENERAL INFORMATION:
;  APPLICANT: Mittmann
;  APPLICANT:  Affymetrix, Inc.
;  TITLE OF INVENTION: Methods of Genetic Analysis of the Rat
;  TITLE OF INVENTION:  Genome
;  FILE REFERENCE: 3112
;  CURRENT APPLICATION NUMBER: US/09/954,427
;  CURRENT FILING DATE:  2001-09-17
;  NUMBER OF SEQ ID NOS: 420907
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 30098
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Rattus norvegicus
;  PUBLICATION INFORMATION:
;   DATABASE ACCESSION NUMBER: GenBank AA818650
US-09-954-427-30098

  Query Match             73.3%;  Score 13.2;  DB 36;  Length 25;
  Best Local Similarity   66.7%;  Pred. No. 5.3e+03;
  Matches   12;  Conservative    3;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 AAUGGCCUAUCGGUGCGA 18
              ||:|| |:|:||| || |
Db          8 AATGGTCTATCGGCGCAA 25


RESULT 11
US-09-956-584-426597/c
; Sequence 426597, Application US/09956584
; GENERAL INFORMATION:
;  APPLICANT: Mittman, Michael
;  TITLE OF INVENTION: Methods of Genetic Analysis of Mus Musculus
;  FILE REFERENCE: 3115.1
;  CURRENT APPLICATION NUMBER: US/09/956,584
;  CURRENT FILING DATE:  2001-09-19
;  PRIOR APPLICATION NUMBER: 60/234,017
;  PRIOR FILING DATE: 2000-09-20
;  NUMBER OF SEQ ID NOS: 605887
;  SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 426597
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Mus musculus
US-09-956-584-426597

  Query Match             73.3%;  Score 13.2;  DB 36;  Length 25;
  Best Local Similarity   66.7%;  Pred. No. 5.3e+03;
  Matches   12;  Conservative    3;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 AAUGGCCUAUCGGUGCGA 18
              || | ||:|:|||: |||
Db         21 AACGACCTATCGGTCCGA 4


RESULT 12
US-09-956-604-6465/c
; Sequence 6465, Application US/09956604
; GENERAL INFORMATION:
;  APPLICANT: Mittmann, Michael
;  TITLE OF INVENTION: Methods of Genetic Analysis of Escherichia coli
;  FILE REFERENCE: 3117.1
;  CURRENT APPLICATION NUMBER: US/09/956,604
;  CURRENT FILING DATE:  2001-09-19
;  PRIOR APPLICATION NUMBER: 60/234,049
;  PRIOR FILING DATE: 2000-09-19
;  NUMBER OF SEQ ID NOS: 141629
;  SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 6465
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Escherichia coli
US-09-956-604-6465

  Query Match             73.3%;  Score 13.2;  DB 36;  Length 25;
  Best Local Similarity   61.1%;  Pred. No. 5.3e+03;
  Matches   11;  Conservative    4;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 AAUGGCCUAUCGGUGCGA 18
              ||:|| |:|:|| :| ||
Db         23 AATGGTCTATCGTTGAGA 6


RESULT 13
US-09-956-604-105593/c
; Sequence 105593, Application US/09956604
; GENERAL INFORMATION:
;  APPLICANT: Mittmann, Michael
;  TITLE OF INVENTION: Methods of Genetic Analysis of Escherichia coli
;  FILE REFERENCE: 3117.1
;  CURRENT APPLICATION NUMBER: US/09/956,604
;  CURRENT FILING DATE:  2001-09-19
;  PRIOR APPLICATION NUMBER: 60/234,049
;  PRIOR FILING DATE: 2000-09-19
;  NUMBER OF SEQ ID NOS: 141629
;  SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 105593
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Escherichia coli
US-09-956-604-105593

  Query Match             73.3%;  Score 13.2;  DB 36;  Length 25;
  Best Local Similarity   61.1%;  Pred. No. 5.3e+03;
  Matches   11;  Conservative    4;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 AAUGGCCUAUCGGUGCGA 18
              | :||||:|:| |:|| |
Db         20 AGTGGCCTATCAGTGCCA 3


RESULT 14
US-09-956-604-114271/c
```

```
; Sequence 114271, Application US/09956604
; GENERAL INFORMATION:
;  APPLICANT: Mittmann, Michael
;  TITLE OF INVENTION: Methods of Genetic Analysis of Escherichia coli
;  FILE REFERENCE: 3117.1
;  CURRENT APPLICATION NUMBER: US/09/956,604
;  CURRENT FILING DATE:  2001-09-19
;  PRIOR APPLICATION NUMBER: 60/234,049
;  PRIOR FILING DATE: 2000-09-19
;  NUMBER OF SEQ ID NOS: 141629
;  SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 114271
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Escherichia coli
US-09-956-604-114271

  Query Match             73.3%;  Score 13.2;  DB 36;  Length 25;
  Best Local Similarity   61.1%;  Pred. No. 5.3e+03;
  Matches   11;  Conservative    4;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 AAUGGCCUAUCGGUGCGA 18
              | :||||:|:|| : |||
Db         20 AGTGGCCTATCGCTACGA 3


RESULT 15
US-09-956-604A-6465/c
; Sequence 6465, Application US/09956604A
; GENERAL INFORMATION:
;  APPLICANT: Mittmann, Michael
;  TITLE OF INVENTION: Methods of Genetic Analysis of Escherichia coli
;  FILE REFERENCE: 3117.1
;  CURRENT APPLICATION NUMBER: US/09/956,604A
;  CURRENT FILING DATE:  2001-09-19
;  PRIOR APPLICATION NUMBER: 60/234,049
;  PRIOR FILING DATE: 2000-09-19
;  NUMBER OF SEQ ID NOS: 141629
;  SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 6465
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Escherichia coli
US-09-956-604A-6465

  Query Match             73.3%;  Score 13.2;  DB 36;  Length 25;
  Best Local Similarity   61.1%;  Pred. No. 5.3e+03;
  Matches   11;  Conservative    4;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 AAUGGCCUAUCGGUGCGA 18
              ||:|| |:|:|| :| ||
Db         23 AATGGTCTATCGTTGAGA 6


Search completed: July  6, 2003, 16:29:55
Job time : 1953.09 secs
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: July 6, 2003, 14:51:21 ; Search time 624.545 Seconds
(without alignments)
206.249 Million cell updates/sec

Title: US-09-780-929-98
Perfect score: 18
Sequence: 1 aauggccuaucggugcga 18

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 8255821 seqs, 3578102051 residues

Total number of hits satisfying chosen parameters: 9359164

Minimum DB seq length: 0
Maximum DB seq length: 60

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending_Patents_NA_New:*
1: /cgn2_6/ptodata/2/pna/PCT_NEW_COMB.seq:*
2: /cgn2_6/ptodata/2/pna/PCT_NEW_COMB.seq4:*
3: /cgn2_6/ptodata/2/pna/US06_NEW_COMB.seq:*
4: /cgn2_6/ptodata/2/pna/US06_NEW_COMB.seq4:*
5: /cgn2_6/ptodata/2/pna/US07_NEW_COMB.seq:*
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9: /cgn2_6/ptodata/2/pna/US09_NEW_COMB.seq:*
10: /cgn2_6/ptodata/2/pna/US09_NEW_COMB.seq2:*
11: /cgn2_6/ptodata/2/pna/US09_NEW_COMB.seq3:*
12: /cgn2_6/ptodata/2/pna/US09_NEW_COMB.seq4:*
13: /cgn2_6/ptodata/2/pna/US10_NEW_COMB.seq:*
14: /cgn2_6/ptodata/2/pna/US10_NEW_COMB.seq2:*
15: /cgn2_6/ptodata/2/pna/US10_NEW_COMB.seq3:*
16: /cgn2_6/ptodata/2/pna/US10_NEW_COMB.seq4:*
17: /cgn2_6/ptodata/2/pna/US60_NEW_COMB.seq:*
18: /cgn2_6/ptodata/2/pna/US60_NEW_COMB.seq2:*
19: /cgn2_6/ptodata/2/pna/US60_NEW_COMB.seq3:*
20: /cgn2_6/ptodata/2/pna/US60_NEW_COMB.seq4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
c	1	13.8	76.7	30	15	US-10-336-566-21	Sequence 21, Appl
	2	13.8	76.7	30	15	US-10-336-566-22	Sequence 22, Appl
c	3	13.2	73.3	24	14	US-10-310-188-56966	Sequence 56966, A
	4	13.2	73.3	25	18	US-60-427-808-19526	Sequence 19526, A
c	5	13.2	73.3	25	18	US-60-427-808-125229	Sequence 125229,
	6	13.2	73.3	25	18	US-60-427-808-897906	Sequence 897906,
	7	13.2	73.3	25	20	US-60-475-871-64253	Sequence 64253, A
	8	13.2	73.3	28	15	US-10-287-787-12927	Sequence 12927, A
	9	13.2	73.3	43	15	US-10-287-787-21425	Sequence 21425, A
	10	13.2	73.3	48	15	US-10-287-787-4996	Sequence 4996, Ap
	11	13	72.2	25	14	US-10-355-577-821852	Sequence 821852,
c	12	13	72.2	25	18	US-60-427-808-512279	Sequence 512279,
c	13	12.8	71.1	25	11	US-09-954-445A-39955	Sequence 39955, A
	14	12.8	71.1	25	14	US-10-355-577-133076	Sequence 133076,
c	15	12.8	71.1	25	14	US-10-355-577-152466	Sequence 152466,
	16	12.8	71.1	25	14	US-10-355-577-703461	Sequence 703461,
c	17	12.8	71.1	25	14	US-10-355-577-834630	Sequence 834630,
	18	12.8	71.1	25	14	US-10-355-577-904618	Sequence 904618,
	19	12.8	71.1	25	18	US-60-427-808-56539	Sequence 56539, A
	20	12.8	71.1	25	18	US-60-427-808-238519	Sequence 238519,
	21	12.8	71.1	25	18	US-60-427-808-304674	Sequence 304674,
c	22	12.8	71.1	25	18	US-60-427-808-534678	Sequence 534678,
c	23	12.8	71.1	25	18	US-60-427-808-547438	Sequence 547438,
c	24	12.8	71.1	25	18	US-60-427-836-69606	Sequence 69606, A
c	25	12.8	71.1	25	18	US-60-427-836-81651	Sequence 81651, A
	26	12.8	71.1	25	18	US-60-427-836-204586	Sequence 204586,
c	27	12.8	71.1	25	18	US-60-427-836-658226	Sequence 658226,
c	28	12.8	71.1	25	19	US-60-469-545-81455	Sequence 81455, A
c	29	12.8	71.1	25	19	US-60-469-545-81457	Sequence 81457, A
c	30	12.8	71.1	25	19	US-60-469-545-82435	Sequence 82435, A
	31	12.8	71.1	25	19	US-60-469-545-155742	Sequence 155742,
	32	12.8	71.1	25	19	US-60-469-545-156720	Sequence 156720,
	33	12.8	71.1	25	19	US-60-469-545-156722	Sequence 156722,
	34	12.4	68.9	25	12	US-09-660-080B-18293	Sequence 18293, A
	35	12.4	68.9	25	14	US-10-355-577-565114	Sequence 565114,
	36	12.4	68.9	25	18	US-60-427-808-918802	Sequence 918802,
	37	12.4	68.9	25	18	US-60-427-836-63726	Sequence 63726, A
c	38	12.4	68.9	25	18	US-60-427-836-165832	Sequence 165832,
	39	12.4	68.9	25	20	US-60-475-871-111969	Sequence 111969,
	40	12.2	67.8	25	11	US-09-954-445A-10275	Sequence 10275, A
	41	12.2	67.8	25	14	US-10-355-577-446254	Sequence 446254,
	42	12.2	67.8	25	14	US-10-355-577-501905	Sequence 501905,
c	43	12.2	67.8	25	14	US-10-355-577-650463	Sequence 650463,
c	44	12.2	67.8	25	14	US-10-355-577-732834	Sequence 732834,
c	45	12.2	67.8	25	14	US-10-355-577-742769	Sequence 742769,

ALIGNMENTS

RESULT 1
US-10-336-566-21/c
; Sequence 21, Application US/10336566
; GENERAL INFORMATION:
; APPLICANT: Robinson, Harriet L.
; APPLICANT: Smith, James M.
; APPLICANT: Hua, Jian
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR GENERATING
; TITLE OF INVENTION: AN IMMUNE RESPONSE
; FILE REFERENCE: 12804-006001
; CURRENT APPLICATION NUMBER: US/10/336,566
; CURRENT FILING DATE: 2003-01-03
; PRIOR APPLICATION NUMBER: US 10/093,953
; PRIOR FILING DATE: 2002-03-08
; PRIOR APPLICATION NUMBER: US 09/798,675
; PRIOR FILING DATE: 2001-03-01
; PRIOR APPLICATION NUMBER: PCT/US01/06795
; PRIOR FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: US 60/251,083
; PRIOR FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: US 60/186,364
; PRIOR FILING DATE: 2000-03-02
; PRIOR APPLICATION NUMBER: US 60/324,845
; PRIOR FILING DATE: 2001-09-25
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-10-336-566-21

Query Match 76.7%; Score 13.8; DB 15; Length 30;
Best Local Similarity 64.7%; Pred. No. 9.6e+02;

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  Matches   11;  Conservative    4;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 AUGGCCUAUCGGUGCGA 18
              |:||| :|:|| :||||
Db         25 ATGGCGTATCGATGCGA 9


RESULT 2
US-10-336-566-22
; Sequence 22, Application US/10336566
; GENERAL INFORMATION:
;  APPLICANT: Robinson, Harriet L.
;  APPLICANT:  Smith, James M.
;  APPLICANT:  Hua, Jian
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR GENERATING
;  TITLE OF INVENTION:  AN IMMUNE RESPONSE
;  FILE REFERENCE: 12804-006001
;  CURRENT APPLICATION NUMBER: US/10/336,566
;  CURRENT FILING DATE:  2003-01-03
;  PRIOR APPLICATION NUMBER: US 10/093,953
;  PRIOR FILING DATE: 2002-03-08
;  PRIOR APPLICATION NUMBER: US 09/798,675
;  PRIOR FILING DATE: 2001-03-01
;  PRIOR APPLICATION NUMBER: PCT/US01/06795
;  PRIOR FILING DATE: 2001-03-02
;  PRIOR APPLICATION NUMBER: US 60/251,083
;  PRIOR FILING DATE: 2000-12-01
;  PRIOR APPLICATION NUMBER: US 60/186,364
;  PRIOR FILING DATE: 2000-03-02
;  PRIOR APPLICATION NUMBER: US 60/324,845
;  PRIOR FILING DATE: 2001-09-25
;  NUMBER OF SEQ ID NOS: 87
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 22
;   LENGTH: 30
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Primer
US-10-336-566-22

  Query Match             76.7%;  Score 13.8;  DB 15;  Length 30;
  Best Local Similarity   64.7%;  Pred. No. 9.6e+02;
  Matches   11;  Conservative    4;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 AUGGCCUAUCGGUGCGA 18
              |:||| :|:|| :||||
Db          6 ATGGCGTATCGATGCGA 22


RESULT 3
US-10-310-188-56966/c
; Sequence 56966, Application US/10310188
; GENERAL INFORMATION:
;  APPLICANT: RosettaGemonics
;  TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENE
;  TITLE OF INVENTION:  USES THEREOF
;  FILE REFERENCE: 47487
;  CURRENT APPLICATION NUMBER: US/10/310,188
;  CURRENT FILING DATE:  2002-12-19
;  NUMBER OF SEQ ID NOS: 86841
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 56966
;   LENGTH: 24
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-310-188-56966

  Query Match             73.3%;  Score 13.2;  DB 14;  Length 24;
  Best Local Similarity   61.1%;  Pred. No. 2.1e+03;
  Matches   11;  Conservative    4;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 AAUGGCCUAUCGGUGCGA 18
              ||:||||:|: | :|| |
Db         21 AATGGCCTATGGATGCAA 4


RESULT 4
US-60-427-808-19526
; Sequence 19526, Application US/60427808
; GENERAL INFORMATION:
;  APPLICANT: Xue Mei Zhou
;  TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
;  FILE REFERENCE: 3528
;  CURRENT APPLICATION NUMBER: US/60/427,808
;  CURRENT FILING DATE:  2002-11-20
;  NUMBER OF SEQ ID NOS: 982914
;  SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 19526
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Mus musculus
US-60-427-808-19526

  Query Match             73.3%;  Score 13.2;  DB 18;  Length 25;
  Best Local Similarity   61.1%;  Pred. No. 2.1e+03;
  Matches   11;  Conservative    4;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 AAUGGCCUAUCGGUGCGA 18
              ||: | |:|:|| :||||
Db          2 AATAGTCTATCGTTGCGA 19


RESULT 5
US-60-427-808-125229/c
; Sequence 125229, Application US/60427808
; GENERAL INFORMATION:
;  APPLICANT: Xue Mei Zhou
;  TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
;  FILE REFERENCE: 3528
;  CURRENT APPLICATION NUMBER: US/60/427,808
;  CURRENT FILING DATE:  2002-11-20
;  NUMBER OF SEQ ID NOS: 982914
;  SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 125229
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Mus musculus
US-60-427-808-125229

  Query Match             73.3%;  Score 13.2;  DB 18;  Length 25;
  Best Local Similarity   66.7%;  Pred. No. 2.1e+03;
  Matches   12;  Conservative    3;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 AAUGGCCUAUCGGUGCGA 18
              || ||||:|:| |: |||
Db         22 AAGGGCCTATCAGTACGA 5


RESULT 6
US-60-427-808-897906
; Sequence 897906, Application US/60427808
; GENERAL INFORMATION:
;  APPLICANT: Xue Mei Zhou
;  TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
;  FILE REFERENCE: 3528
;  CURRENT APPLICATION NUMBER: US/60/427,808
;  CURRENT FILING DATE:  2002-11-20
;  NUMBER OF SEQ ID NOS: 982914
;  SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 897906
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Mus musculus
US-60-427-808-897906
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```
  Query Match             73.3%;  Score 13.2;  DB 18;  Length 25;
  Best Local Similarity   66.7%;  Pred. No. 2.1e+03;
  Matches   12;  Conservative    3;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 AAUGGCCUAUCGGUGCCGA 18
              ||:||||  :| |:||||
Db          4 AATGGCCATTCTGTGCGA 21


RESULT 7
US-60-475-871-64253
; Sequence 64253, Application US/60475871
; GENERAL INFORMATION:
;  APPLICANT: Wyeth Research
;  APPLICANT:  Mounts, William M.
;  APPLICANT:  Murphy, Ellen M.
;  TITLE OF INVENTION: Staphylococcus Aureus Nucleic Acid Arrays
;  FILE REFERENCE: AM101085
;  CURRENT APPLICATION NUMBER: US/60/475,871
;  CURRENT FILING DATE:  2003-06-05
;  NUMBER OF SEQ ID NOS: 207175
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 64253
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Staphylococcus aureus
US-60-475-871-64253

  Query Match             73.3%;  Score 13.2;  DB 20;  Length 25;
  Best Local Similarity   66.7%;  Pred. No. 2.1e+03;
  Matches   12;  Conservative    3;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 AAUGGCCUAUCGGUGCGA 18
              | :| || |:|||:||||
Db          4 AGTGTCCAATCGGTGCGA 21


RESULT 8
US-10-287-787-12927
; Sequence 12927, Application US/10287787
; GENERAL INFORMATION:
;  APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
;  TITLE OF INVENTION: Caulobacter crescentus complete genome.
;  FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
;  CURRENT APPLICATION NUMBER: US/10/287,787
;  CURRENT FILING DATE:  2003-03-03
;  NUMBER OF SEQ ID NOS: 27958
;  SOFTWARE: Proprietary
; SEQ ID NO 12927
;   LENGTH: 28
;   TYPE: DNA
;   ORGANISM: Caulobacter crescentus complete genome.
;   FEATURE:
;   LOCATION: (1889626)...(1889653)
;   OTHER INFORMATION: Chromosome = 1  Strand = negative  ConnectronObjectNumber = 14264
US-10-287-787-12927

  Query Match             73.3%;  Score 13.2;  DB 15;  Length 28;
  Best Local Similarity   66.7%;  Pred. No. 2.1e+03;
  Matches   12;  Conservative    3;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 AAUGGCCUAUCGGUGCGA 18
              ||:| ||  :|||:||||
Db          2 AATGCCCGGTCGGTGCGA 19


RESULT 9
US-10-287-787-21425
; Sequence 21425, Application US/10287787
; GENERAL INFORMATION:
;  APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
;  TITLE OF INVENTION: Caulobacter crescentus complete genome.
;  FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
;  CURRENT APPLICATION NUMBER: US/10/287,787
;  CURRENT FILING DATE:  2003-03-03
;  NUMBER OF SEQ ID NOS: 27958
;  SOFTWARE: Proprietary
; SEQ ID NO 21425
;   LENGTH: 43
;   TYPE: DNA
;   ORGANISM: Caulobacter crescentus complete genome.
;   FEATURE:
;   LOCATION: (3144703)...(3144745)
;   OTHER INFORMATION: Chromosome = 1  Strand = positive  ConnectronObjectNumber =
US-10-287-787-21425

  Query Match             73.3%;  Score 13.2;  DB 15;  Length 43;
  Best Local Similarity   66.7%;  Pred. No. 2.2e+03;
  Matches   12;  Conservative    3;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 AAUGGCCUAUCGGUGCGA 18
              ||:| ||  :|||:||||
Db          2 AATGCCCGGTCGGTGCGA 19


RESULT 10
US-10-287-787-4996
; Sequence 4996, Application US/10287787
; GENERAL INFORMATION:
;  APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
;  TITLE OF INVENTION: Caulobacter crescentus complete genome.
;  FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
;  CURRENT APPLICATION NUMBER: US/10/287,787
;  CURRENT FILING DATE:  2003-03-03
;  NUMBER OF SEQ ID NOS: 27958
;  SOFTWARE: Proprietary
; SEQ ID NO 4996
;   LENGTH: 48
;   TYPE: DNA
;   ORGANISM: Caulobacter crescentus complete genome.
;   FEATURE:
;   LOCATION: (733016)...(733063)
;   OTHER INFORMATION: Chromosome = 1  Strand = positive  ConnectronObjectNumber =
US-10-287-787-4996

  Query Match             73.3%;  Score 13.2;  DB 15;  Length 48;
  Best Local Similarity   66.7%;  Pred. No. 2.2e+03;
  Matches   12;  Conservative    3;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 AAUGGCCUAUCGGUGCGA 18
              ||:| ||  :|||:||||
Db          2 AATGCCCGGTCGGTGCGA 19


RESULT 11
US-10-355-577-821852
; Sequence 821852, Application US/10355577
; GENERAL INFORMATION:
;  APPLICANT: Mittmann, Michael
;  TITLE OF INVENTION: Methods of Genetic Analysis of Probes: HG-U133
;  FILE REFERENCE: 3121
;  CURRENT APPLICATION NUMBER: US/10/355,577
;  CURRENT FILING DATE:  2003-01-31
;  NUMBER OF SEQ ID NOS: 997516
;  SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 821852
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Homo sapien
US-10-355-577-821852

  Query Match             72.2%;  Score 13;  DB 14;  Length 25;
  Best Local Similarity   76.9%;  Pred. No. 2.7e+03;
  Matches   10;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          6 CCUAUCGGUGCGA 18
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              ||:|:|||:||||
Db          2 CCTATCGGTGCGA 14


RESULT 12
US-60-427-808-512279/c
; Sequence 512279, Application US/60427808
; GENERAL INFORMATION:
;  APPLICANT: Xue Mei Zhou
;  TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
;  FILE REFERENCE: 3528
;  CURRENT APPLICATION NUMBER: US/60/427,808
;  CURRENT FILING DATE:  2002-11-20
;  NUMBER OF SEQ ID NOS: 982914
;  SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 512279
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Mus musculus
US-60-427-808-512279

  Query Match             72.2%;  Score 13;  DB 18;  Length 25;
  Best Local Similarity   76.9%;  Pred. No. 2.7e+03;
  Matches   10;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AAUGGCCUAUCGG 13
              ||:||||:|:|||
Db         23 AATGGCCTATCGG 11


RESULT 13
US-09-954-445A-39955/c
; Sequence 39955, Application US/09954445A
; GENERAL INFORMATION:
;  APPLICANT: Mittmann, Michael
;  TITLE OF INVENTION: Methods of Genetic Analysis of Arabidopsis Thaliana
;  FILE REFERENCE: 3116.1
;  CURRENT APPLICATION NUMBER: US/09/954,445A
;  CURRENT FILING DATE:  2000-09-17
;  PRIOR APPLICATION NUMBER: 60/233,620
;  PRIOR FILING DATE: 2000-09-18
;  NUMBER OF SEQ ID NOS: 131820
;  SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 39955
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Arabidopsis thaliana
US-09-954-445A-39955

  Query Match             71.1%;  Score 12.8;  DB 11;  Length 25;
  Best Local Similarity   62.5%;  Pred. No. 3.5e+03;
  Matches   10;  Conservative    4;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 AAUGGCCUAUCGGUGC 16
              ||: || :|:|||:||
Db         22 AATTGCATATCGGTGC 7


RESULT 14
US-10-355-577-133076
; Sequence 133076, Application US/10355577
; GENERAL INFORMATION:
;  APPLICANT: Mittmann, Michael
;  TITLE OF INVENTION: Methods of Genetic Analysis of Probes: HG-U133
;  FILE REFERENCE: 3121
;  CURRENT APPLICATION NUMBER: US/10/355,577
;  CURRENT FILING DATE:  2003-01-31
;  NUMBER OF SEQ ID NOS: 997516
;  SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 133076
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Homo sapien
US-10-355-577-133076

  Query Match             71.1%;  Score 12.8;  DB 14;  Length 25;
  Best Local Similarity   68.8%;  Pred. No. 3.5e+03;
  Matches   11;  Conservative    3;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 AUGGCCUAUCGGUGCG 17
              | || |:|:|||:|||
Db          5 AAGGACTATCGGTGCG 20


RESULT 15
US-10-355-577-152466/c
; Sequence 152466, Application US/10355577
; GENERAL INFORMATION:
;  APPLICANT: Mittmann, Michael
;  TITLE OF INVENTION: Methods of Genetic Analysis of Probes: HG-U133
;  FILE REFERENCE: 3121
;  CURRENT APPLICATION NUMBER: US/10/355,577
;  CURRENT FILING DATE:  2003-01-31
;  NUMBER OF SEQ ID NOS: 997516
;  SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 152466
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Homo sapien
US-10-355-577-152466

  Query Match             71.1%;  Score 12.8;  DB 14;  Length 25;
  Best Local Similarity   62.5%;  Pred. No. 3.5e+03;
  Matches   10;  Conservative    4;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          3 UGGCCUAUCGGUGCGA 18
              : | |:|:|||:||||
Db         21 TTGACTATCGGTGCGA 6


Search completed: July  6, 2003, 16:49:14
Job time : 625.545 secs
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